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APPLICANT: Endang, Hong
APPLICANT: Endang, Hong
APPLICANT: Sim, Kim Lee
APPLICANT: Sim, Kim Lee
APPLICANT: Chang-Murad, Amy
APPLICANT: Chang-Murad, Amy
APPLICANT: Chang-Murad, Amy
APPLICANT: Becrnet, Courdes L.
APPLICANT: Bermejo, Lourdes L.
APPLICANT: Schrimmbar, Joeffrey L.
APPLICANT: Joeffrey L.
APPLICANT: Schrimmbar, Joeffrey L.
APPLICANT: Joeffrey L
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Patent No. 672536
GENERAL INFORMATION:
APPLICANT: Madsen, John
APPLICANT: Sim, Kim Lee
APPLICANT: Zim, Kim Lee
APPLICANT: Zhou, Xinhua
APPLICANT: Chang-Murad, Amy
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-377-250-3
US-09-377-250-2
US-08-612-788-42
US-09-066-028-42
US-09-355-614-42
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US-08-451-932-3
US-08-452-260-3
US-08-612-785-3
US-08-612-788-3
US-08-612-788-3
US-08-612-788-3
US-08-66-735-3
US-09-35-513-3
US-09-335-313-3
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US-08-924-287A-1
US-08-924-287A-1
US-08-924-287A-1
US-08-147-000B-29
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US-09-192-012-5
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US-09-192-012-5
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181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
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Pred. No. 1.5e-138;
0; Mismatches 1; Indels
                                                                                                                                                    Sequence 3, Application US/08248629A
Fatent No. 5639725
GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TILLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,629A
FILING DATE: 04/26/94
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05213-0120
                                      241 TNSQVRWEYCKIPSCDSSPV 260
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                                                                        241 TNSQVRWEYCKIPSCDSSPV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: LAITY W. STUILES, Ph.D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 0521:
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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404-818-3799
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Best Local Similarity 99.6'
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                      US-08-248-629A-3
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                                                                                                                                    RESULT 2
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DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
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          Sequence 3, Application US/08451932
Patent No. 5733876
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Method of Treating an Angiogenic TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

99.7%; Score 1535; DB 1;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                               ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,932
FILING DATE: 05/26/95
CLASSIFICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: LAILY W. SLULLS, Ph.D.
REGISTRATION NUMBER: 34,025
REGISTRATION NUMBER: 34,025
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 34,025
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US-08-452-260-3
'Sequence 3, Application US/08452260
'Patent No. 5776704
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TELEPHONE: 404-818-3700
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US-08-451-932-3
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CORRESPONDENCE ADDRESS
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99.6%; Pred. No. 1.5e-138;
tive 0; Mismatches 1; Indels
                      APPLICANT: POLICALION:

APPLICANT: PO'Really, Michael
TITLE OF INVENTION: Method of Diagnosing an Angiogenic
TITLE OF INVENTION: Method of Diagnosing and Angiogenic
TITLE AT ALLanta
STREET: 191 Peachtree Street, 37th Floor
CUNTRY: USA
ZIP: 30303-1769
CONFUTE: Georgia
CONFUTE: Macintosh
OORPUTE: Macintos
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PAMENT NO. 5792845
GENERAL INFORMATION:
APPLICANT: FOLKman, Judah
APPLICANT: O'Reilly, Michael
APPLICANT: O'Reilly, Michael
NUMBER OF INVENTION: Angiostatin and Method of Use
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.69
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-452-260-3
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US-08-326-785-3
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61 DPQGPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GYIPSKFPNKALKKAYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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; Sequence 3, Application US/08612788
; Sequence 3, Application US/08612788
; Patent No. 2813/682
; GENERAL INFORMATION:
; APPLICANT: C'REALLY, Micheal
; APPLICANT: Cao, Yihai
; APPLICANT: O'REALLY, Micheal
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCES ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use
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ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1769
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: MacIntosh
                                                                                                                                                                                                                  COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,785
                                                                                                                                                                                                                                                                                                                                                      PILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,629
FILING DATE: 04/26/94
ATVOREY/ABONT INFORMATION:
NAME: LARTY W. Stults, Ph. D.
REGISTRATION NUMBER: 34,025
REFERENCE/DOCKET NUMBER: 05213-01
TELECHONNICATION INFORMATION:
TELECHONS: 404-818-3790
INFORMATION FOR SEQ ID NO: 3:
ERGURENCE CHARACTERISTICS:
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TNSQVRWEYCKIPSCDSSPV 260
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Matches 259; Conservative
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TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6
Matches 259; Conservative
                  STATE: Georgia
CCUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-605-598B-3
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Setent No. 5861372
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
APPLICANT: O'Reilly, Michael S.
TITLE OF INVENTION: Aggregate Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnes & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                CONDITY: U.S.

CUDNITY: U.S.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TYPE: AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.7%; Score 1535; DB 1;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNSQVRWEYCKIPSCDSSPV 260
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CLONE: Angiostatin fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-605-598B-3
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181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT 240
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CURPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,598B
FILING DATE: 22-PEB-196
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WATEN, WILLIAM L.
REGISCOMMUNICATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
TELEPRATION NUMBER: 36,714
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATION 1870-1999
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APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
APPLICANT: Sim, Kim Lee
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 99.6%; Pred. No. 1.5e-138; Obs. Conservative 0; Mismatches 1;
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Patent No. 5885795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Human Angiostatin
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us-09-502-176-2.rai

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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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US-09-066-028-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GYIPSKPPNKOLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DPQGPWCYTTDPEKRYDYCDILLECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1535; DB 1;
Pred. No. 1.5e-138;
0; Mismatches 1;
                                                                                                                                                              FILING DATE:
CLASSISTICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACELES:
                                                                                                                                                                                                                                                                                                                                                                                                                05213-0122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
30303-1769
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61 DPQGPWCYTTDPEKRYDYCDILECERECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GYIPSKPPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VYLSECKTGNGKNYRGTWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PRILICATION NUMBER: US/08/866,735 FILING DATE: 30-MAY-1997 CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.7%; Score 1535; DB 1;
Best Local Similarity 99.6%; Pred. No. 1.5e-138;
Matches 259; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TNSQVRWEYCKIPSCDSSPV 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (404) 818-3700
TELERAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDENNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPQGPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERIPENFPCKNLDENYCRNPDGKRAPWCHT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                     ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1535; DB 2;
Pred. No. 1.5e-138;
0; Mismatches 1;
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                  05213-0126
                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TNSQVRWEYCKIPSCDSSPV 260
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                                                                                                                                                                                                                                                                                                                                                       NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE, DOCKET NUMBER: 05213
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPAX: 404-818-3700
TELEPAX: 404-818-3700
TELEPAX: 404-818-3700
TELEPAX: 439-818-3799
INPORMATION FOR SEQ ID NO: 3: SEQUENCE GHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
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Patent No. 6521439
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.78;
                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                        Georgia
: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                      Atlanta
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61 DPQGP#CYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GYIPSKPPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 99.6%; Pred. No. 1.5e-138; 59; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
FILING DATE: «Unknown»
ATTORNEY AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REGISTRATION NUMBER: 36,714
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <UNKNOWD>
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TNSQVRWEYCKIPSCDSSPV 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-818-3799 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                   ZIP: 30303-1769
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Simil
Matches 259; C
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RESULT 12 US-09-335-614-3

APPLICANT: Folkman, M. Judah O'Reilly, Micheal Cao, Yihai

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61 DPQGPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGKISKTWSGLECQAWDSQSPHAH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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                                                                                                                                                                                            Sequence 3, Application PC/TUS9505107
GENERAL INFORMATION:
APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION
TITLE OF INVENTION: Anglostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ALLanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 33033-176
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1535; DB 5;
Pred. No. 1.5e-138;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELEPHONE: 404-818-3700
      241 TNSQVRWEYCKIPSCDSSPV 260
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Best Local Similarity 99.6
Matches 259; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 404-818-379:
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: HOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                    PCT-US95-05107-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-05107-3
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                                                                                                                                             RESULT 13
                                               셤
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Sequence 3, Application US/09335614
Patent No. 6949511
GENERAL INFORMATION:
GRAFICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Georgia
COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRNT APPLICATION DATA:
APPLICATION DATR:
FILING DATE: 18-Jun-1999
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-335-614-3
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Patent No. 6365364

GENERAL INFORMATION:

APPLICANT: SMORDS JENNY, NANCY

TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF

FILE REFERENCE: 48409/360

CURRENT APPLICATION NUMBER: US/09/377,250

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                GENERAL INFORMATION:
APPLICANT: MANN, KENNETH G.
APPLICANT: SWARDS JENNY, NANCY
APPLICANT: SWARDS JENNY, NANCY
TITLE OF INVENTION UNMERS: US/09/377,250
CURRENT APPLICATION NUMBER: US/09/377,250
CURRENT PAPLICATION NUMBER: 1999-08-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1535; DB 2;
Pred. No. 1.7e-138;
0; Mismatches 1;
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TYPE: PRT
TYPE: PRT
TYPE: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: angiogenesis inhibitor
                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: MOD RES

LOCATION: (264)

OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-3
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US-09-377-250-3; Sequence 3, Application US/09377250; Patent No. 6365364
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Best Local Similarity 99.6%;
Matches 259; Conservative (
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61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
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                                                                                                                         Length 375;
                                                                                                                                                              Indels
                                                                                                                   Query Match 99.7%; Score 1535; DB 2;
Best Local Similarity 99.6%; Pred. No. 1.7e-138;
Matches 259; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: August 29, 2006, 14:02:54 Job time : 50 secs
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (265)
; OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2
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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

August 29, 2006, 13:53:08; Search time 299 Seconds (without alignments)
804.361 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-502-176-2 1540 1 VYLSECKTGNGKNYRGTMSK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table:

2849598 seqs, 925015592 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P00747 homo sapien Q5teh4 homo sapien Q5teh4 homo sapien Q5teh4 homo sapien P12545 macaca mula P12545 macaca mula Q8wmr1 canis famil Q0117 rattus norv Q5bkb6 rattus norv P06867 sus scrofa P6686 hos taurus Q6tci0 mus musculu Q29488 erinaceus e Q7tp84 rattus norv O18798 ariacopus eu Q6ba6 poracropus eu Q6ba6 prachydanio Q29488 erinaceus e Q50146 mus musculu Q28398 erinaceus e Q6gp14 xenopus lae Q6gp14 xenopus lae P1210 homo sapien Q7ztn9 xenopus lae P1210 homo sapien Q7ztn9 xenopus lae P17945 rattus norv Q90978 gallus gallu Q867b7 canis famil Q867b7 canis famil Q867b7 canis famil Q86948 mus musculu Q5346 mus musculu	9
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DB		4
Length	810 810 810 810 812 812 812 812 812 812 812 812	3
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Score	1535 1535 1535 1535 1539 1299 1299 1299 1279 1279 1279 1279 127	?
Result No.		1

Q76bs1 bos taurus Q90865 gallus gall Q9bb09 felis silve G5rgg3 brachydanio Q5xfy1 brachydanio Q90zn6 brachydanio P70521 rattus norv Q4rx92 tetraodon n Q3uz05 mus musculu Q78862 gallus gall P26928 mus musculu Q6gt11 m macrophag Q91xg8 mus musculu Q6gt11 w macrophag
0768S1 BOVIN 090865_CHICK 090809_FELCA 090809_FELCA 05RGG3_BRARE 090ZN6_BRARE P70521_RAT 04RX92_TETNG 03UZ05_MOUSE 078802_CHICK HGFL MOUSE 06GTL1_MOUSE 091XG8_MOUSE
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## ALIGNMENTS

RESULT 1 PLAN HUMAN  ALD PLAN HUMAN  ALD PLAN DD  DT 01-JU  DT 01-JU  DD 01-JU  RA PETER  RA PETER  RA PETER  RA PETER  RA POLIS  RA RIEGE  RA RIE
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RRITER BERKEREN BERKER BERKEREN BERKER BERK
RA Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards K., Wuzny D.M., Sodercen E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Ra Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

RT and mouse CDNA sequences.";
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Malinowski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sottrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.; "The primary structure of human plasminogen."; [II] Davidson J.F., Rowan R.M., Samama M.M., Davidson J.F., Rowan R.M., Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810, AND VARIANT
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"Amino-acid sequence of the cyanogen-bromide fragment from human wanino-acid sequence of the linkage between the plasmin chains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mary structure of the B-chain of human plasmin."; J. Biochem. 76:129-137(1977).
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Submitted (JUL-1977) to the PIR data bank.
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MEDLINE=82213905; PubMed=6919539;
RA Pratchenko L., Marusina K., Farmer RA Bronaten M.J., Usdin T.B., Monaldo Bronaten M.J., Usdin T.B., Bonaldo RA Raha S.S., Loquellano N.A., Peters RA Raha S.S., Loquellano N.A., Peters Bosak S.A., McDawan P.J., McKernan R. A., Milaino D.K., Warzy D.M., Sodargre RA Aniting M., Madan A., Young A.C., Shakesley W. Milting M., Madan A., Young A.C., Slakesley R.W., Touchman J.W., Grencration and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and mouse cDNA sequences.; Procentation and initial analysis of and and soft. D. Petersen T.B., McCherry Jensen L., Petersen T.B., McLarchtractation of a complementary allowed and bowine plasminogen.; Procentations between '9 wiman and bowine plasminogen.'; Progress in chemical fibrinolysis a setuctive of the cyanoge RY Develorem. Sol. 489-494 (1975). RN '8 wiman B., Wallen P.; Rowan R.M., Sam RY CHINES SEQUENCE OF 55-580; SBL-626 ASN-472. RN '8 man B., Wallen P.; Rowan R.M., Sam Progress in chemical fibrinolysis and plasmino-acid sequence of the Gyanoge RY The primary structure of the B-chain of RY Progress in chemical fibrinolysis and Progress of a percentage of the cyanoge RY Man B., Wallen P.; Rowan R.M., Summan B., Wallen P.; Robbins K.C., Bernabe P., Azadon L. (11) RY PROTEIN SEQUENCE OF 581-591-547 (1975). RN PROTEIN SEQUENCE OF 581-591-547 (1975). RN PROTEIN SEQUENCE OF 581-591-547 (1975). RN PROTEIN SEQUENCE OF Sell-810.

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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Rnsembl; ENSG000012194; Homo sapiens.

Go; GO:0008230; F:aclium ion binding; IEA.

Go; GO:0008231; F:peptidase activity; IEA.

Go; GO:0008231; F:peptidase activity; IEA.

Go; GO:0008231; F:plasmin activity; IEA.

Go; GO:0008231; F:plasmin activity; IEA.

Go; GO:0008781; F:plasmin activity; IEA.

Go; GO:0008781; F:peptidase IEA.

InterPro; IPR000001; Kringle.

R InterPro; IPR001369; Pan_app.

R InterPro; IPR001369; Pept ElA Plasmin.

R InterPro; IPR001354; Peptidase S1 S6.

InterPro; IPR001354; Peptidase S1A.

InterPro; IPR001364; Peptidase S1A.
                                                          1; Indels
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                Score 1535; DB 1;
Pred. No. 4.9e-109;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                           QSTEH4_HUMAN PRELIMINARY; PRT; QSTEH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PLG; ORFNames=RP1-81D8.1-001;
Biochemistry 30:10576-10588(1991)
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Pfam; pro0024; BrN 1; 1.

Pfam; pro0089; Trypsin; 1.

PIKSF; PIRSPO01150; Plasmin; 1.

PRINTS; PR00722; CHYMOTRYSIN.

PRINTS; PR001018; KRINGLE.

PRINTS; PR01505; PROTHROMBIN.
                                  Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative
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21-DEC-2004, sequence version 1.
21-DEC-2006, entry version 12.
Hypothetical protein DKFZp470G2422.
Name=DKFZp470G2422;
Pongo pygmaeus (Orangutan).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae,
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The German CDNA Consortium;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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SMR; Q5R8K6; 185-352, 564-810.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004283; F:peptidase activity; IEA.
GO; GO:0007596; P:blosmin activity; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
GO; GO:000580; P:proteolysis; IEA.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; Pan.
InterPro; IPR003014; Pan.
SMART; SM00130; KR; 5.

SMART; SM0043; PAN AP; 1.

SMART; SM00020; TryP_SPc; 1.

PROSITE; PSS0070; KRINGLE_2; 5.

PROSITE; PSS0040; PAN; 1.

PROSITE; PSS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DM; 1.

PROSITE; PS00134; TRYPSIN LHS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN LHS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN LHS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN SR; 1.

PHYDROLOGE; PS00135; TRYPSIN SR; 1.
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99.6%; Pred. No. 4.9e-109;
tive 0; Mismatches 1;
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Matches 259; Conservative
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                                                                                                                                                                                                                                                                                             218 GYIPSKPPNKNIKKNYCRNPDGEPRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 277
                                                                                                                                                                                                                                                                                                             GTGENYRGNVAVTVSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                                                                                                                                                                                                                                                                                                     278 GTGENYRGNVAVTVSGHTCQRWSAQTPQTHNRTPENFPCKNLDENYCRNPDGEKAPWCYT 337
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158 DAQCPWCYTTDPEHRYDYCDIPECEEACMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                    1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                               GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989, integrated into UniProtKB/Swiss-Prot.
01-OCT-1989, sequence version 1.
07-MAR-2006, entry version 63.
Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A, short form; Plasmin light
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                                                                                                                                                                                                    Gaps
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89174660; PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites
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                                                                                                                                                                                     Length 810;
                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                     94.7%; Score 1458; DB 2;
95.0%; Pred. No. 3.8e-103;
live 3; Mismatches 10;
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                                                                                                                                                                                            Best Local Similarity 95.0 Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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GYIPSKPPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                         01-MAR-2002, integrated into UniProtKB/TrEMBL.
01-MAR-2002, sequence version 1.
07-FBB-2006, entry version 18.
Plasminogen (Fragment).
Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE. Paria-Sepapherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O., Polkman J., Waters D.J.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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R HSSP; P00747; 1PMK.

R ENREL; AY069985; AAL58519.1; -; mRNA.

R GWMRI, 187-255.

R GO; GO:0005509; F:calcium ion binding; IRA.

GO; GO:0007550; F:sacrium-type endopeptidase activity; IEA.

GO; GO:0007550; F:sacrine-type endopeptidase activity; IEA.

GO; GO:0000550; F:sproded coaqulation; IRA.

R GO; GO:0000550; F:proded coaqulation; IRA.

R GO; GO:0000508; F:proteolysis; IRA.

InterPro; IPR000001; Kringle.

R InterPro; IPR00001; Kringle.

R PRINTS; PR0018; KRINGLE.

R PRINTS; PR01505; PROTHROMBIN.

R PRODM; PR000139; KRINGLE.

R PROSTIE; SM00130; KR; 4.

R PROSTIE; PS50070; KRINGLE 1; 4.
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81.2%; Pred. No. 6.9e-92;
ative 23; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 AA; 41173 MW; 776D35F4AB0BDD9E CRC64;
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TNSEVRWEHCQIPSCESSPI 260
                      241 TNSOVRWEYCKIPSCDSSPV 260
                                           338 TNSQVRWEYCKIPSCESSPV 357
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QBWMRI CANFA
QBWMRI;
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                                                                                short form.
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93.6%; Score 1442; DB 1; Length 810;
Best Local Similarity 93.1%; Pred. No. 6.4e-102;
Matches 242; Conservative 9; Mismatches 9; Indels
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Omega-aminocarboxylic acids.
Omega-aminocarboxylic acids.
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                                   Activation peptide.
/FTId=PRO 000028061.
/FTId=PRO 0000028062.
Plasmin light chain B.
Plasmin heavy chain A. /FIId=PRO 0000028060.
                                                                                                                                   'FTId=PRO 0000028063
                                                                                                                                                                                                                                                                                            Charge relay system.
Charge relay system.
Charge relay system.
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RESULT 6

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                                                                             EMBL; M62832; AAA41884.1; -; mRNA
PIR; A40522; A40522.
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                                                                                                                                                                                                                                                                           InterPro; IPR000001; Kringle.
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**Ranalas J.J. Makker S.P.;

**Ranalas J.J. Makker S.P.;

**Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor site for plasminogen.";

**Leceptor site for plasminogen.";

**Leceptor Sec.: 10825-10829 (1991).

**Leceptor Sec.: 10825-10829 (1991).

**Leceptor Sec.: 10825-10829 (1991).

**Leceptor Processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as Cland CS. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG4.

**Leceptor Sec.: 108701.** Angiostatin is an angiogenesis inhibitor that blocks necvasication and growth of experimental primary and metastatic tumors in vivo (By similarity).

**Leceptor Sec.: 108701.** Argulation in vivo (By similarity).

**Leceptor Sec.: 108701.** Argulation in vivo (By similarity).

**Leceptor Sec.: 108701.** Argulation in trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-581, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity)

MSCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

MISCELLANEOUS: In the presence of the inhibitor, the activation involves anly cleavage after Arg-581, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide (By
                                                                                                                                                                                                                                        Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B].
                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria, Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
SUBUNIT: Interacts with CSPG4 and ANOT (By similarity).
SUBCELLULAR LOCATION: Secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver;
Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure ";
Submitted (MAX-1999) to the EMBL/Genbank/DDBJ databases.
                                                                    PLANN RAT

ID PLAN RAT

AC 001177; Q9R0W3;
DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.
DT 31-A06-2004, sequence version 2.
DT 31-A06, notry version 60.
DT 07-MAR-2006, entry version 60.

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-!- SIMILARITY: Contains 1 PAN domain.
-!- SIMILARITY: Contains 1 peptidase 51 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA] OF 343-511.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                 Name=Plg;
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Blood coagulation; Fibrinolysis; Hydrolase; Kringle; Protease; Repeat;
Serine protease; Signal; Tissue remodeling; Zymogen.
SIGNAL 1 19 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTIGHERO 0000028079.
Plasmin heavy chain A.
/FTIGHERO 0000028080.
Activation peptide (By similarity).
/FTIGHERO 0000028081.
Plasmin heavy chain A, short form.
/FTIGHERO 0000028082.
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(By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiostatīn.
/FTId=PRO_0000028083.
Plasmin līght chain B.
/FTId=PRO_000028084.
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SMR; Q01177; 565-812.
MEROPS; S01.237; -.
MEROPS; S01.233; -.
RGD; 619893; P1g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen.
                                                                                                                                                      InterPro; IPR003609; Pan app.
InterPro; IPR01358; Pept SIA Plasmin.
InterPro; IPR01358; Pept SIA Plasmin.
InterPro; IPR01254; PeptIdase SI.S6.
InterPro; IPR001254; PeptIdase SIA.
InterPro; IPR003966; Peptidase SIA.
Pfam; PF00051; Kringle; 5.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; TryPsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR01505; PROTHROMBIN.
PRINTS; PR01505; PROTHROMBIN.
PRODOM; PD0001395; Kringle; 1.
SWART; SM00130; KR; 5.
SWART; SM00020; TryP_SPC; 1.
PROSTITE; PS00021; KRINGLE.; 5.
PROSTITE; PS00021; KRINGLE.; 5.
PROSTITE; PS00021; KRINGLE.; 5.
EMBL; AJ242649; CAB46014.1; -; mRNA
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A Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Haich F.,

A Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Rapleton M., Joace M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunzratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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                                                                                                                                                                                                                                                                                                                                                                 218 GYIPAKFPSKNLKMNYCRNPDGEPRPWCFTTDPNKRWBYCDIPRCTTPPPPPPGPTYQCLK 277
                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                             DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen.
Name=Plg;
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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By similarity.
By similarity.
By similarity.
By similarity.
Interchain (between A and B chains) (B similarity).
Interchain (between A and B chains) (B similarity).
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TISSUB=Liver;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                   84.4%; Score 1299; DB 1; Length 812;
                                                                                                                                                                               82.6%; Pred. No. 5.8e-91;
ive 21; Mismatches 24; Indels
                                                                                                                                  A -> S (in Ref. 2).
8C703C51410EBC9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-WAY-2005, integrated into UniProtKB/TrEMBL. 10-WAY-2005, sequence version 1. 07-FBB-2006, entry version 10.
                                                                                        By similarity.
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By similarity.
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TDSQLRWEYCEIPSCGSS 355
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                                                                                                                                              90536 MW;
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108 213; Conservative
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SEQUENCE
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            ISULPID
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                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 VYLSECKTGIGKGYRGTMSKTKTGVTCQKWSDTSPHVPKYSPSTHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 DEQCPWCYTTDPDQRXEYCNIPECEECMYCSGEKYEGKISKTMSGLDCQSWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            # SWR (JERGES) 555-812.

# GO; GO:0005509; F:calcium ion binding; IEA.

# GO; GO:0004283; F:plasmin activity; IEA.

# GO; GO:0004283; F:plasmin activity; IEA.

# GO; GO:000508; P:proteolysis; IEA.

# InterPro; IPR00001; Kringle.

# InterPro; IPR00149; PAN.

# InterPro; IPR0013609; Pan.app.

# InterPro; IPR0013609; Pan.app.

# InterPro; IPR001354; Peptidase_81_86.

# InterPro; IPR001369; Peptidase_81_86.

# InterPro; IPR001369; Peptidase_81_86.

# InterPro; IPR001369; Peptidase_81_86.

# Perpro; IPR001369; Peptidase_81_86.

# Perpro; IPR001369; Peptidase_81_86.

# Perpro; IPR001369; Peptidase_81_86.

# Perpro; PR001269; PR0THROMBIN.

# PRINTS; PR00136; KR. 56.

# PRNTS; PR000473; PR0THROMBIN.

# PRNTS; PR000473; PR0THROMBIN.

# PRNTS; PR000473; PR0THROMBIN.

# PROSITE; PS00021; TRNTGLE_1; UNKNOWN_5.

# PROSITE; PS00021; TRNTGLE_2; 5.

# PROSITE; PS00021; TRNTGLE_2; 5.
                                                                                                                                                                                                                                                    NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50948; PAN; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS502134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
Hydrolase; Kringle; Protease; Serine protease.
AROHENCE 812 AA; 90536 MW; 8C703C51410EBC9E CRC64;
                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.4%; Score 1299; DB 2;
82.6%; Pred. No. 5.8e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.6%; Pred. No. 5.8e ive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC091135; AAH91135.1; -; mRNA.
SMR; Q5BKB6; 565-812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNSOVRWEYCKIPSCDSS 258
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TDSQLRWEYCEIPSCGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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/FTIGLEGR 000020.
By similarity.
                                                                 HSSP, P00747, IBUI.
SMR; P00667; 544-790.
MEMOPS, 501.233.
GLYCOSUIteDB; P06867; -.
InterPro; IPR001001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR00314; PAN.
InterPro; IPR001358; Pept SIA Plasmin.
InterPro; IPR001358; Pept SIA Plasmin.
InterPro; IPR001354; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR003966; Peptidase SIA.
                                                                                                                                                                                                                                                                                        PRINTS; PRO0722; CHYMOTREPEIN.
PRINTS; PRO1018; KRINGLE.
PRINTS; PRO1018; KRINGLE.
PROD001; PRO11019; KR.
SMART; SM00130; KR; 5.
SMART; SM00473; PAN AP; 1.
SMART; SM00020; TYP_SPC; 1.
PROSITE; PS00021; KRINGLE 1; 5.
                                                                                                                                                                                                                                 Pfam; PF00051; Kringle; 5.
Pfam; PF000051; PAN 1; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001150; Plasmin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue remodeling; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      790
                                                        PIR; S03733; PLPG.
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MEDLINE=88185329; PubMed=3356193;
A Marti T., Schaller J., Rickli B.B., Schmid K., Kamerling J.P.,
A Gerwig G.J., van Halbeek H., Vliegenthart J.P.,
Gerwig G.J., van Halbeek H., Vliegenthart J.P.,
The N- and O-linked carbohydrate chains of human, bovine and porcine
T plasminogen. Species specificity in relation to sialylation and
fucosylation patterns.;
T Eur. J. Biochem. 173:57-63(1988).
C --- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
c embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovulation it weakens the walls of the Graafian
c collagenases and several complement zymogens, such as Cl and CS.
It cleaves fibrin, fibronectin, thrombospondin, laminin and von
Willebrand factor. Its role in tissue remodeling and tumor
invasion may be modulated by CSPG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purillarity).

PTM: N-linked glycan contains N-acetyllactosamine, sialic acid and is core fucosylated. O-linked glycans consist of Gal-GalNAc disaccharide which is modified with up to 2 sialic acid residues (microheterogeneity).

PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-560, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the
                                                                                                                                                                                                                                                Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli B.B.; *Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the carbohydrate attachment sites with the human and bovine
                                      01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
01-FRB-1991, sequence version 2.
07-MAR-2006, entry version 66.
Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activation involves addditionally the removal of the activation peptide (By similarity).
MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENCYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with Streptokinase.
SUBUNIT: Interacts with CSP64 (By similarity).
SUBCELLULAR LOCATION: Secreted protein.
DOMAIN: Kringle domains mediate interaction with CSP64 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immediately after dissociation from the clot. SIMILARITY: Belongs to the peptidase SI family. Plasminogen
                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85203907; PubMed=3846533;
Marti T., Schaller J., Rickli E.E.;
"Determination of the complete amino-acid sequence of porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 5 kringle domains.
-!- SIMILARITY: Contains 1 PAN domain.
-!- SIMILARITY: Contains 1 peptidase S1 domain.
             790 AA
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 149:279-285(1985)
                                                                                                                                                                                                                                                                                            species.";
Fibrinolysis 1:91-102(1987).
                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 450-790
                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                   PROTEIN SEQUENCE OF 1-560.
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               miniplasminogen.";
                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                                                   Schaller J
             PLMN PIG
                                                                                                                                 Name=PLG;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50070; KRINGLE_2; S.
PROSITE; PS5040; TRYPSIN DOM; 1.
PROSITE; PS50140; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; PALSE NEG.
PROSITE; PS00135; TRYPSIN HIS; L.
Blood coagulation; Direct protein sequencing; Fibrinolysis;
Glycoprotein; Hydrolase; Kringle; Protease; Repeat; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmin heavy chain A.
/Fride-PRO 000028075.
/Fride-PRO 0000028076.
Plasmin heavy chain A, short form.
/Fride-PRO 000028077.
Plasmin light chain B.
/Fride-PRO 0000028077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kringle 1.
Kringle 2.
Kringle 3.
Kringle 4.
Kringle 5.
Peptidase S1.
Charge relay system.
Charge relay system.
Charge relay system.
N-linked (GLONAc. . .).
FridacAR 000019.
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                                                                                                                                                                                                               GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                                                                                                                                                                                                                                                                           79 IYLSECKTGNGKNYRGTTSKTKSGVICQKWSVSSPHIPKYSPEKFPLAGLEENYCRNPDN 138
                                                                                                                                                                                                     61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                           121 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                9
                                                                                                                                                               1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDÉTINE-85023311; PubMed-6148961;
Malinôwski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasminogen precursor (BC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A, short form; Plasmin light
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Complete amino acid sequence of bovine plasminogen. Comparison with
                              (B)
                                                (B)
 By similarity.
By similarity.
By similarity.
Interchain (between A and B chains)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Bukaryota; Metasoca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Luarasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinee; Bos.
                                     similarity).
Interchain (between A and B chains)
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85203906; PubMed=3846532;
Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J.,
Kampfer U., Rickli B.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berglund L., Andersen M.D., Petersen T.E.; "Cloning and characterization of the bovine plasminogen cDNA."; Int. Dairy J. 5:593-603(1995).
                                                                                                                                            ö
                                                                                                                          Length 790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES
                                                                                                                                           25; Indels
                                                                                             / similarity.
F04EA06E74BCD58E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               P06867 (228162)
01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
01-NOV-1997, sequence version 2.
07-MAR-2006, entry version 68.
                                                                                                                         DB 1;
                                                                                                                         Score 1292; DB 1;
Pred. No. 1.9e-90;
                                                                By similarity.
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                          812 AA
                                                                                                                                            23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] OF 706-812.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bur. J. Biochem. 149:267-278(1985)
                                                                                                                                                                                                                                                                                                                                 319 TDSEVRWDYCKIPSCGSS 336
                                                                                                                                                                                                                                                                                                                       241 TNSQVRWEYCKIPSCDSS 258
                                                                                                      88593 MW;
                                                                                                                        Query Match
Best Local Similarity 81.4%;
Matches 210; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                           736
790 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human plasminogen.";
                                               557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                         PLMN BOVIN
DISULPID
DISULPID
DISULPID
DISULPID
                                                                           DISULPID
                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PLG;
                                               DISULPID
                                                                 DISULFID
                                                                                                      SEQUENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
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-I- PTM: N-linked glycan contains N-acetyllactosamine and sialic acid.

O-linked glycans consist of Gal-GalNAc disaccharide which is modified with up to 2 slalic acid residues (microheterogeneity).

-I- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-583, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves addditionally the removal of the activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
-I- SUBURIT: Interacts with CSPG4 (By similarity).
-I- SUBCELLULAR LOCATION: Secreted protein.
-I- DOMAIN: Kringle domains mediate interaction with CSPG4 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide (By similarity).
--- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
--- SIMILARITY: Belongs to the peptidase SI family. Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1-SIMILARITY: Contains 5 kringle domains.
-1-SIMILARITY: Contains 1 PAN domain.
-1-SIMILARITY: Contains 1 peptidase S1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003609; Pan app. Flagmin. InterPro; IPR011358; Pept S1A Plasmin. InterPro; IPR001254; Peptidase_S1_S6. InterPro; IPR001314; Peptidase_S1A. InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X79402; CAA55939.1; -; mRNA.
EMBL; K02935; AAA30714.1; -; mRNA.
                                                                                                           MEDLINE=88185329; PubMed=3356193;
uman and bovine plasminogen.";
iochemistry 23:4243-4250(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIRSF; PIRSF001150; Plasmin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01505; PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000395; Kringle; 5.
SMART; SM00130; KR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00051; Kringle; 5. Pfam; PF00024; PAN 1; 1. Pfam; PF00089; Trypsin; 1.
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SMR; P06868; 568-812.
MEROPS; S01.233; -.
                                                                                    CARBOHYDRATE-LINKAGE
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120

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225 GYIPSKFPNKNLKANYCRNPDGEPRPWCFTTDPQKRWEFCDIPRCTTPPPSSGPKYQCLK 284
                                                                                                                                                                                                                                                                                                                     285 GTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENYCRNPNGEKAPWCYT 344
                                                                                                                                                                                                121 GYIPSKEPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                            181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                          Name=pig;
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
    VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                   DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
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RSP; P00747; 1B21.

RG; GO:0005576; C:extracellular region; RCA.

GO; GO:0005576; C:extracellular region; RCA.

GO; GO:0005515; P:horporcas; IDA.

GO; GO:0006515; P:horporcas; IDA.

GO; GO:006515; P:nogration of apoptosis; IDA.

GO; GO:004576; P:mescle maintenance; IMP.

InterPro; IPR003004; PAN.

RITHERPO; IPR003066; Peptidase_SIA_PP.

RPINTS; PR00018; KRINGLE;

RRINTS; PR00018; KRINGLE;

RRART; SM00130; KR; 4.

RRART; SM00130; KRINGLE 1; 4.

RRART; SM00131; KRINGLE 1; 4.

RRART; SM00131; KRINGLE 1; 4.

RRAINGLE; PSS0010; KRINGLE 2; 4.

RRAINGLE 3.

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Qiao H., Tang B., Sun X.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004, integrated into UniProtXB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 15. Anglostatin.
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QGTCIO;
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MWART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50048; PAN; 1.
PROSITE; PS50040; TRYPSIN_DOM; 1.
PROSITE; PS50040; TRYPSIN_DOM; 1.
PROSITE; PS500134; TRYPSIN_BIS; 1.
PROSITE; PS001134; TRYPSIN_BIS; 1.
Blood coagulation; Direct protein sequencing; Fibrinolysis; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease;
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                                                                                                                                                                                                                                                                                            Plasminogen.
/Frida-PRO 000028039.
Plasmin heavy chain A.
/Frida-PRO 000028040.
/Frida-PRO 0000028041.
/Frida-PRO 0000028041.
Plasmin heavy chain A, short form (By
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80.8%; Pred. No. 2.4e-90;
:ive 23; Mismatches 27; Indels
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Kringle 2.
Kringle 3.
Kringle 4.
Kringle 5.
Peptidase S1.
Charge relay system.
Charge relay system.
Charge relay system.
Ylinked (GLOMAC. . .).
/FTIGHCAR 000014.
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Plasmin light chain B.
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SIGNAL 1 26
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Best Local Similarity 80.8°
Matches 210; Conservative
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                                                                                                                    61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                    158 DEQGFWCYTTDPDKRYDYCNIPECEEECMYCSGEKYEGKISKTWSGLDCQAWDSQSPHAH 217
                                                                                                                                                                           121 GYIPSKPPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                         218 GYIPAKFPSKNLKANYCRNPDGEPRPWCFTTDPTKRWEYCDIPRCTTPPPPPSSPTYQCLK 277
                                                                                                                                                                                                                                  181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                                                                                                                                                                                                                                278 GRGENYRGIVSVIVSGKICQRWSEQIPHRHRRIPENFPCKNLEENYCRNPDGETAPWCYT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Atlauner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Rasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worlfey K.C., Hale S., Garcia A.M., Gibbs R.A., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu, Gibbs R.A., Rahey'J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                  9
                                                                1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B].
                                      Gaps
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
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Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
"Characterization of the cDNA coding for mouse plasminogen and localization of the gene to mouse chromosome 17.";
Genomics 8:49-61(1990).
          Query Match
83.1%; Score 1279; DB 2; Length 466;
Best Local Similarity 81.0%; Pred. No. 1.1e-89;
Matches 209; Conservative 22; Mismatches 27; Indels (
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01-PBE-1991, integrated into UniProtKB/Swiss-Prot.
30-MAX-2003, sequence version 2.
07-MAR-2006, entry version 76.
                                                                                                                                                                                                                                                                                                                                                                                       812 AA
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/PITd=PRO 000028069.
Plasmin heavy chain A.
/FITd=PRO 0000028070.
Activation peptide.
/FITd=PRO_000028071.
Plasmin heavy chain A, short form.
/FITd=PRO_0000028072.
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Plasmin light chain B.
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Kringle 2.
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Kringle 5.
Peptidase S1.
Charge relay system (1
Charge relay system (1
Charge relay system (1
Sharge relay system (1
Sharmlarity.
                  MEROPS; S01.233; -.
Ensembl; ENSMUSG0000059481; Mus musculus.
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STRAIN=CS7BL/6J; TISSUE=Placenta and extra embryonic tissue;

STRAIN=CS7BL/6J; TISSUE=Placenta and extra embryonic tissue;

Rubmed=16.41072; DOI=10.1126/science.1112014;

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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Interchain (between A and B chains)
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; Pred. No. 2e-89;
22; Mismatches 27; Indels
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GO; GO:0066915; P:normone activity; RCA.
GO; GO:0045945; P:nordottion of apoptosis;
GO; GO:0045246; P:myoblast differentiation
GO; GO:0016525; P:megative regulation of
GO; GO:0012246; P:tissue regeneration; IM
InterPro; IPR00001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR011358; Pept SIA Plasmin.
InterPro; IPR011358; Pept SIA Plasmin.
InterPro; IPR001344; Peptidase SI S6.
InterPro; IPR001314; Peptidase SI S6. EMBL; AK132254; BAE21060.1; -; mRNA. Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE 

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07-MAR-2006, entry version 52.
Plasminogen precursor (8C 3.4.21.7) [Contains: Plasmin heavy chain A, Activation peptide; Plasmin heavy chain A, short form; Plasmin light
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Insectivora; Brinaceidae;
Brinaceinae; Erinaceus
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00134; TRYPBIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
MterPro, IPR003966; Peptidase SIA pp.
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J. Biol. Chem. 270:24004-24009(1995).
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       PEAM; PF00051; Kringle; S.
PEAM; PF00024; PAM 1; 1.
PIRSF, PIRSF001150; Plasmin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR001050; RRINGLE.
PRINTS; PR001055; PROTHOWBIN.
PRODOM; PD000395; KRINGLE.
SWART; SW00403; RR; S.
SWART; SW00403; PR, S.
PROSITE; PS00020; TryD SPC; 1.
PROSITE; PS00021; KRINGLE 1; S.
PROSITE; PS50070; KRINGLE 1; S.
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                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLMN ERIEU
029485;
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PRINTS; PRO0125; CHYMOTRYBEIN.

R PRINTS; PRO0125; CHYMOTRYBEIN.

R PRINTS; PRO0136; KRINGLE.

R Process PRO0136; Kringle; 5.

SMART; SM00473; PAN AP; 1.

SMART; SM00473; PAN AP; 1.

SMART; SM0020; Tryp_SPc; 1.

R PROSITE; PS50070; KRINGLE 1; 5.

R PROSITE; PS50070; KRINGLE 2; 5.

R PROSITE; PS50040; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN BR; 1.

R PROSITE; PS00135; TRYPSIN BR; 1.

R PROSITE; PS00135; TRYPSIN SR; 1.

R PROSITE; PS00135; TRYPSIN SR; 1.

R PROSITE; PS00135; TRYPSIN SR; 1.

R PROCESS PS0014 DOM; 1.

R PROCESS PS0015; TRYPSIN SR; 1.

R PROCESS PS0015; TRYPSIN SR; 1.

R PROCESS PS0016 PS0015; TRYPSIN SR; 1.
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                               a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG. CATALTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-58, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves addditionally the removal of the activation
FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
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Plasmin heavy chain A (By similarity).
FVId=PRO 000028047.
Activation peptide (By similarity).
/FVId=PRO_000028048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
-!- SUBGNIT: Interacts with CSPG4 (By similarity).
-!- SUBGLIULAR LOCATION: Secreted protein.
-!- DOMAIN: Kringle domains mediate interaction with CSPG4 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide (By similarity).
--- MISCELANBOORS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
--- SIMILARITY: Belongs to the peptidase SI family. Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 5 kringle domains.
-!- SIMILARITY: Contains 1 PAN domain.
-!- SIMILARITY: Contains 1 peptidase 51 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasminogen.
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InterPro; IPR011358; Pept S1A Plasmin.
InterPro; IPR001254; Pept Tdase_S1_86.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR003966; Peptidase_S1A.pp.
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PIR; I46260; I46260.
MSSP; POO747; IBUI.
SMR; Q29485; 568-810.
MEROPS; S01.233; -.
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Pfam; PF00024; PAN 1; 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001150; Plasmin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 DPQGPWCYTTDPEKRYDYCDILLECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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By similarity.
                                            Kringle 1.
Kringle 2.
Kringle 3.
Kringle 4.
Kringle 5.
Peptidase S1.
Charge relay system.
Charge relay system.
Charge relay system.
Charge relay system.
       similarity).
/FrId=PRO_000028049.
Plasmin light chain B (By similarity)
/FrId=PRO_000028050.
                                                                                                                                                                                                                                                                                      and B chains)
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 Plasmin heavy chain A, short form
                                                                                                                                                                                                                                                                                                                                                  80.3%; Score 1237; DB 1; Length 810; 77.9%; Pred. No. 3.2e-86; ive 26; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                            Bimilarity.
8E75780946017A16 CRC64;
                                                                                                                                                                                                                                                                              similarity).
Interchain (between A
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By similarity.
By similarity.
By similarity.
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Les 201; Conservative
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729
756
810 AA;
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CARBOHYD
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PRT;

PRELIMINARY;

RESULT 14 Q7TP84 RAT; ID. Q7TP84 RAT AC. Q7TP84;

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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota, Metazoa Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
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                                                                                                                                                                                                                                                                                                                                                                                                  Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma Wang L., Wang i.L.Q., Yuan J.Y., Yang K.J., Shi J.B., Rahman S.; Wang Q.N., Zhang J.B., Submitted (JUN-2003) to the RMBL/GenBank/DDBJ databases.
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HSSP; P00747; 1BUI.

SWR; QYTP64; 83-360, 661-75.

R Ensembl; ENSRNGG00000017223; Rattus norvegicus.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005283; F:plasmin activity; IEA.

GO; GO:0005284; P:proteolysis; IEA.

GO; GO:0005509; P:proteolysis; IEA.

GO; GO:0005509; P:proteolysis; IEA.

R GO; GO:0005014; PRO.

R InterPro; IPR001359; Pept SlA Plasmin.

R InterPro; IPR001359; PeptIdase_Sl_S6.

R InterPro; IPR001359; PeptIdase_Sl_Dp.

R Ffam; PR00024; PAN_1; 1.

R PRINTS; PR00150; PROTHROWBIN.

R PRINTS; PR00130; Kringle; 5.

R SWART; SW000130; KRINGLE.

R PROSITE; PS50001; KRINGLE.

R PROSITE; PS50010; TRYPEIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 78.1%; Score 1203.5; DB 2; Length Local Similarity 71.1%; Pred. No. 1.1e-83; hes 204; Conservative 22; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTPENFPCKNLDENYCRNPDGKRAPWCHTTNSQVRWEYCKIPSCDSS
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01-OCT-2003, integrated into UniProtXB/TrEMBL, 01-OCT-2003, sequence version 1. 07-PEB-2006, entry version 16.
                                                                                                                                                                                                                                                                                                                                                                       NUCLEÒTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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TISSUB-Liver;

WEDLINE=98004511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;

X Lawn R.M., Schwartz K., Patthy L.;

Lawn R.M., Schwartz K., Patthy L.;

Lawn R.M., Schwartz K., Patthy L.;

Loonvergent evolution of apolipoprotein(a) in primates and hedgehog.";

Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).

-:- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian CC inflammation; in ovulation it weakens the walls of the Graafian CC inflammation; in ovulation it weakens the walls of the Graafian CC inflammation; in coulain the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as Cl and CS.

It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor CC willebrand factor. Its role in tissue remodeling and tumor CC introduction may be modulated by CSFG4 (By similarity).

CC --- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa, Arg-|-Xaa, higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                         31-AUG-2004, integrated into UniProtKB/Swiss-Prot. 01-7AN-1998, sequence version 1. 07-MAR-2006, entry version 40. Plasminogen precursor (82 3.4.21.7) [Contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A, short form; Plasmin light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).

PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-576, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANDENCE Planning in inactivated by alpha-2-antiplasmin immediately after dissociation from the clot (By similarity). MISCELLANDENCE: In the presence of the inhibitor, the activation involves only cleavage after Arg-576, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase (By similarity)
                                                                                                                                                                        Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Interacts with CSPG4 (By similarity).
SUBCELLULAR LOCATION: Secreted protein.
DOMAIN: Kringle domains mediate interaction with CSPG4 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eubfamily.
-!- SIMILARITY: Contains 5 kringle domains.
-!- SIMILARITY: Contains 1 PAN domain.
-!- SIMILARITY: Contains 1 peptidase 51 domain.
                               806 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003609; Pan app.
InterPro; IPR011358; Pept 51A Plasmin.
InterPro; IPR001254; Peptidase SI S6.
InterPro; IPR001314; Peptidase_SIĀ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF012297; AAB65760.1; -; mRNA.
HSSP; P00747; 1BUI.
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA].
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00747; 1BUI.
SMR; O18783; 561-806.
MEROPS; S01.233; -.
                                                                                                                                                                                                                      NCBI_TaxID=9315;
                            PLMN MACEU
                                                                                                                                            chain B].
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              MACEU
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PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PRO0122; CHYMOTRYPSIN.

PRINTS; PRO0132; CHYMOTRYPSIN.

PRINTS; PRO1505; PROTHROMEIN.

PROD0315; Kringle; 5.

R PARAT; SM0043; PAN_AP; 1.

SMART; SM00473; PAN_AP; 1.

SMART; SM0020; TRYP_SIN.

PROSITE; PS50040; KRINGLE 1; 5.

PROSITE; PS50040; TRYPSIN DOM; 1.

PROSITE; PS50134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

R Serine proclease; Signal; Tissue remodeling; Zymogen.

T SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                  plasmin heavy chain A (By similarity)
/FTIG=PRO 0000028065.
Activation peptide (By similarity).
/FTIG=PRO_0000028066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=PRO 0000028067.
Plasmin līght chain B (By similarity)
/FTId=PRO_0000028068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmin heavy chain A, short form (By
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similarity).
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Interchain (between A and B chains)
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95FAA86DC20064D5 CRC64;
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Kringle 2.

Kringle 3.

Kringle 4.

Kringle 5.

Peptidase S1.

Charge relay system (B Charge relay system (B S similarity).

By similarity.

By similarity.
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71.7%; Pred. No. 2.5e-80;
ive 34; Mismatches 39;
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By similarity.
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By similarity
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InterPro; IPR003966; Peptidase_S1A_pp.
                 Pfam; PF00051; Kringle; 5.
Pfam; PF000024; PAN 1.
Pfam; PF00089; Trypsin; 1.
PIRSF; PIRSF001150; Plasmin; 1.
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Gaps

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39; Indels

Search completed: August 29, 2006, 14:01:16 Job time : 302 secs

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

August 29, 2006, 13:56:28; Search time 39 Seconds (without alignments) 641.445 Million cell updates/sec

Title: Perfect score:

US-09-502-176-2 1540 1 VYLSBCKTGNGKNYRGTMSK......TNSQVRWEYCKIPSCDSSPV 260 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	TO 3.4.21	_	_			plasmin (EC 3.4.21	apolipoprotein(a)	hepatocyte growth	hepatocyte growth		hepatocyte growth	macrophage-stimula	hepatocyte growth	macrophage-stimula	apoprotein(a) (EC	macrophage-stimula	apolipoprotein(a)			ρ,		쁘	thrombin (BC 3.4.2	thrombin (BC 3.4.2	thrombin (BC 3.4.2	t-plasminogen acti	t-plasminogen acti	t-plasminogen acti	plasmin (EC 3.4.21
SUMMARIBS	PLHII	B30848	PLPG	PLBO	PLMS	146260	T18518	JH0579	A35644	151283	A60185	JC5061	I51285	A40332	800657	A47136	A32869	A61545	B61545	533879	TBBO	A40522	A35827	TBHU	S10511	UKHUT	A35029	A29941	B61545
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* Query Match Length	810	810	790	812	812	810	2869	728	728	710	728	716	411	716	4548	711	1420	455	460	336	625	169	618	622	617	562	559	559	120
% Query Match	99.7	93.6	83.9	83.8	82.7	80.3	57.2	51.8	50.8	50.4	50.4	49.8	49.0	48.9	48.6	48.0	48.0	32.8	32.4	25.4	24.2	23.5	23.2	22.8	22.6	20.1	19.2	18.3	18.1
Score	1535	1442	1292	1291	1274	1237	881	797	782	776.5	116	766.5	754.5	753.5	749	739	739	505	499	391.5	372	362.5	357.5	351	348	309.5	255.5	281.5	278
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plasmin (EC 3.4.21	plasmin (EC 3.4.21	neurotrophic recep	neurotrophic recep	ror-related recept	coagulation factor	plasma hyaluronan-	plasma hyaluronan-	t-plasminogen acti	coagulation factor	coagulation factor	hepatocyte growth	hypothetical prote	u-plasminogen acti	u-plasminogen acti	u-plasminogen acti
A60140	C61545	A45082	B45082	A47299	S28941	JC5878	JC4795	138098	KFHU12	\$45281	A46688	T18840	JN0560	UKPG	S18932
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83	123	937	943	946	603	558	260	291	615	593	655	908	433	442	432
17.6	17.4	15.7	15.6	15.4	15.1	13.9	13.6	13.1	12.9	12.4	12.2	11.6	10.7	6.6	9.8
271	268	241.5	240	237.5	233	214	210	201	198	190.5	188.5	178.5	165	153	151
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1	plasmin (BC 3.4.21.7) precursor [validated] - human	N,Alternate names: plasminogen precursor [misnomer]	N, Contains: angiostatin, microplasmin, plasminogen	C;Species: Homo sapiens (man)	C;Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004	C; Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A046	R; Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.	J. Biol. Chem. 265, 6104-6111, 1990	A; Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibri	A; Reference number: A35229; MUID:90202879; PMID:2318848	A;Accession: A35229	A;Molecule type: DNA	A;Residues: 1-810 <pet></pet>	A; Cross-references: UNIPROT: P00747; UNIPROT: Q9UBQ9; UNIPROT: Q9UMI2; UNIPARC: UPI000016AEC5	A; Experimental source: leukocyte; lung fibroblast	R; Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Tar	Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990	A; Title: Definition of the transcription initiation site of human plasminogen gene in liv	

A;Accession: I52242
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.16 < MALI>
A;Residues: 1.16 < MALI>
A;Residues: 1.16 < MALI>
A;Cross-references: UNIPARC: UPI0000062A8; GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g
B;Porsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FERS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human planamer az6646; MuID:87162490; PMID:3030813
A;Accession: A26646.

A; Molecule type: mRNA
A; Residues: 1-471, 'D', 473-810 <FOR>
A; Cross-references: 10-471, 'D', 473-810 <FOR>
A; Cross-references: UNIPARC: UP10000000BBB; GB: X05199; NID: G35530; PIDN: CAA28831.1; PID: G2
A; Experimental source: 11ver
R; Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry, 23, 4243-4250, 1984
A; Title: Characterization of a complementary deoxyribonucleic acid coding for human and b
A; Reference number: 145961; MUID: 85023311; PMID: 6148961

A Accession: 162738 A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA A;Residues: 292-471, D',473-810 <MAL2> A;Cross-references: UNIPARC:UP100016AED4; GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g A;Accession: I84609

A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 367-419 cMAL3.
A;Residues: 367-419 cMAL3.
A;Cross-references: UNIPARC:UP10000071C7D; GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:
Extransholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, B.B.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, h

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A;Reference number: A65803; PDB:1HPJ
A;Reference number: A65803; PDB:1HPJ
A;Contents: annotation; conformation by (1)H-NWR, residues 103-181
R;Rejante, M.; Llinas, M.
Submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65804; PDB:1HPR
A;Contents: annotation; conformation by (1)H-NWR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Bur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NWR assignments and secondary structure of human plasminogen kringle 1.
R;Rejante, M.R.; Llinas, M.
Bur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
C;Comment: Plasminogen is sonverted to plasmin by plasminogen activators (see PIR:UKHU ar depsilon-aminohem: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU ar depsilon-aminohem: Allaminogen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Contents: authorized, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I. Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
A;Reference number: A39483; MUID:92118803; PMID:1310033
A;Reference number: A39483; MUID:92118803; PMID:1310033
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
B;Reference number: A65800; PDB:1KRN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Reference number: A65803; PDB:1KRN
B;Reference number: A65803; PDB:1HPJ
A;Reference number: A65803; PDB:1HPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R; Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A; Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 An A; Reference number: A58819; MUID: 92031502; PMID: 1657148
A; Contents: annotation
Biochemistry 30, 10589-10594, 1991
A; Title: The refined structure of the epsilon-aminocaproic acid complex of human plasminc A; Reference number: A8818; MUID: 92031503; PMID: 1657149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a var as the walls of the graafian follicle; also activates the urokinase-type plasminogen acti A; Pathway: fibrinolysis C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately aft rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor, C.Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial condi C.Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Togting solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529/
                                                                                                                                                                                                                    A;Contents: annotation; X ray crystallography, 2.48 angstroms, residues 102-181 R;Padmanabhan, K.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank, April 1994 A;Reference number: A52408; PDB:1PMK
                                      A; Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454 R; Wu, T.P.; Tulinsky, A. submitted to the Brookhaven Protein Data Bank, August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                          residues 377-454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues
                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation; X-ray crystallography, 2.25 angstroms, R;Tulinsky, A.; Mathews, I.I. submitted to the Brookhaven Protein Data Bank, December 1995 A; Reference number: A65244; PDB:1CEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Contents: annotation; X-ray crystallography, 2.1 angstroms, R;Tullinsky, A.; Mathews, I.1. submitted to the Brookhaven Protein Data Bank, December 1995 A;Reference number: A65245; PDB:1CEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:119498; OMIM:173350
                                                                                                                                                                                  A; Reference number: A51911; PDB:1PKR
    A; Reference number: A51488; PDB:2PK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 6q26-6q27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 581-810 <WI1>
A;Cross-references: UNIPARC:UP100001450E9
K;Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP10000172B8E
R;Wiman, B.; Wallen, P.
Bur. J. Biochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha A;Reference number: A04626; MUID:76043692; PMID:126863
A;Accession: A04626
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A;Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A;Reference number: A92125; MUID:73149248; PMID:4694729
A;Contents: annotation; active site
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B;Gloskopf, W.R.; Summaria, L.; Robbins, K.C.
A;Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A;Reference number: A92048; MUID:69234739; PMID:4240117
A;Contents: annotation; active site
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J. Biol. Chem. 257, 7401-7406, 1982
A; Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A; Reference number: A92382; MUDD:82213905; PMD:6919539
A; Contents: annotation; omega-aminocarboxylic acid binding sites
R; Vali, Z.; Patthy, L.
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A; Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A; Reference number: A92458; MUD:85054794; PMID:6094526
A; Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R; Cao, Y; Ji, RW, ; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
Biol. Chem. 271, 23461-23467, 1996
A; Title: Kringle domains of human angiostatin. Characterization of the anti-proliferativ
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Biochemistry 37, 4699-4702, 1998
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 A;Reference number: A58812; WUID:9548733; PMID:9548733
A;Contents: annotation
R;Tulinsky, A.; Mulichak, A.W.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51341; PDB:1PK4
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R;Tulinsky, A.; Wu, T.P.
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
A;Cross-references: UNIPARC:UP1000017288D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UP10000172B8D
R;Wiman, B.
Bur: J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
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    number: S03735; MUID:81212097; PMID:7238497
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A;Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2>
A;Cross-references: UNIPARC:UPI0000172B8E
                                                                                      A; Molecule type: protein
A; Residues: 20-71, E', 73-76 <BRU>
A; Cross-references: UNIPARC:UP10000172B8C
R; Sottrup-Jensen, L.; Petersen, T.E.; Magnusson,
submitted to the Atlas, July 1977
A; Reference number: A00929
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Residues: 483-507, E',509-604 <WI3>
Cross-references: UNIPARC:UPI0000172B8F
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277

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NyAlternate names: plasminogen
NyContains: miniplasminogen
Cypecies: Sus scrofa domestica (domestic pig)
Cypecies: Sus scrofa dos (domestic pig)
RySchaller, U.; Marti, T.; Roesselet, S.U.; Kaempfer, U.; Rickli, B.B.
Fibrinolysis I, 91-102, 1987
A; Fibrinolysis I, 91-102, 1987
A; Fibrinolysis I, 91-102, 1087
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A;Molecule type: Lectin
A;Residues: 1-560 -6SGH>
A;Residues: 1-560 -6SGH>
A;Cross-references: UNTPROT:P06867; UNIPARC;UPI0000172890
B;Cross-references: University P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Bur. J. Blocchem. 114, 465-470, 1891
Bur. J. Blocchem. 114, 465-470, 1891
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, the A;Reference number: S03735; MUID:81212097; PMID:7238497
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A;Pathway: fibrinolysis
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F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B #status experimental <BCH>
F;561-790/Product: plasmin chain B #status experimental <BCH>
F;561-790/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-
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Bur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A;Reference number: A25834; MUID:85203907; PMID:3846533
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F;1-77/Domain: activation peptide #status predicted <APT>
F;78-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;66-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;256-335/Domain: kringle homology <KR3>
F;256-335/Domain: kringle homology <KR4>
F;256-335/Domain: kringle homology <KR4>
F;256-336/Domain: kringle homology <KR4>
F;256-350/Domain: kringle homology <KR4>
F;256-3
      158 DGOGPWCYTTDPERRPDYCDIPECEDECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 217
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                                                                                                                                                                                                                                                                                                         218 GYIPSKFPNKNLKKNYCRNPDGEPRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
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A;Residues: 1-57 <BRU>
A;Cross-references: UNIPARC:UP10000172B91
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A;Residues: 450-790 <MAR>
A;Cross-references: UNIPARC:UP10000172B92
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Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #text_change 09-Jul-2004
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5557-5965, 1989
J. Biol. Chem. 264, 5557-5965, 1989
J. A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 DPQGPWCYTTDPEKRYDYCDILECEEBCMHCSGBNYDGKISKTWSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGENYRGNVAVIVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT
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                                                   F;1-96/Domain: plasminogen-related protein precursor howology «PLPH»:
F;1-19/Domain: signal sequence #status predicted «SIG»
F;20-810/Product: plasminogen #status experimental «PRO»
F;20-96/Domain: activation peptide #status experimental (APT»
F;79-466/Product: angiostatin #status experimental «AST»
F;97-886,SB1-810/Product: plasmin #status experimental «MAT»
F;97-580/Domain: plasmin chain A #status experimental «CHA»
F;91-810/Domain: kringle homology «KRI»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.7%; Score 1535; DB 1; Length 810; Best Local Similarity 99.6%; Pred. No. 1.6e-104; Matches 259; Conservative 0; Mismatches 1; Indels
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Pred. No. 9.4e-98;
9; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNSQVRWEYCKIPSCDSSPV 260
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Best Local Similarity 93.1%;
Matches 242; Conservative
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A;Molecule type: mRNA
A;Residues: 1-810 <TOM>
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81.4%; Pred. No. 8e-87;
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Matches 210;
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A;Cross-references: UNIPROT:P20918; UNIPARC:UPI0000028BF2; GB:J04766; NID:g200402; PIDN:; R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Blochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
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                                                                                                                                                                                                                                                                                                                                                                                                                                           F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,333
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C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: A38514; 848202; §48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott of A;Title: Characterization of the cDNA coding for mouse plasminogen and localization of A;Reference number: A38514; MUID:91184812; PMID:2081600
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experimental <APT>
                                F;104-583,584-812/Product: plasmin #status experimental <MAT>
P;104-583/Domain: plasmin chain A #status experimental <ACH>
P;110-188/Domain: kringle homology <RR1>
P;192-269/Domain: kringle homology <RR2>
P;192-269/Domain: kringle homology <RR3>
P;283-359/Domain: kringle homology <RR3>
P;284-461/Domain: kringle homology <RR3>
P;485-564/Domain: kringle homology <RR5>
P;486-564/Domain: plasmin chain B #status experimental <BCH>
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peptide #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 22-27 <LI2>
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A;Residues: 1-812 <DEG>
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A;Cross-references: UNIPARC:UP10000172B96
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteclytic factor in a vante walls of the graafian follicle; also activates the urokinase-type plasminogen act A;Pathway: fibrinolysis
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A;Residues: 1-812 <BER>
A;Cross.references: UNIPROT:P06868; UNIPARC:UPI0000043BEB; EMBL:X79402; NID:g494962; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Bris. J. Balochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasm
A;Reference number: A25835; MUID:85203906; PMID:3846532
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 706-743, 'R', 745-812 «MAL>
A;Cross-references: UNIPARC:UPI000016C365; GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:
Bibchem: 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A;Reference number: S03735; MUD:81212097; PMID:7238497
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A,Residues: 27-334, D. 334, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
                                                                                                  DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                           GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmin (EC 3.4.21.7) precursor - bovine
N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text_change 09-Jul-2004
C;Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: S45046; A25835; I45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
A;Description: Cloning and characterizatin of the bovine plasminogen cDNA.
A;Reference number: S45046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYLPSKPPNKNLKMNYCRNPDGEPRPKCFTTDPNKRWEFCDIPRCTTPPPTSGPTYQCLK
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F;185-262/Domain: kringle homology
F;275-352/Domain: kringle homology
F;379-456/Domain: kringle homology
F;482-561/Domain: kringle homology
F;582-803/Domain: trypsin homology
                                                                                                                   80.3%;
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Best Local Similarity
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                                                                      A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vans the walls of the graafian follicle; also activates the urokinase-type plasminogen act A; Pathway: fibrinolysis
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F;1-96;Domain: plasminosen-related protein precursor homology <PLPH>
F;1-96;Domain: plasminosen-related protein precursor homology <PLPH>
F;103-181/Domain: kringle homology <KR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin (BC 3.4.21.7) precursor - western Buropean hedgehog
C;Species: Brinaceus europaeus (western Buropean hedgehog)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146260
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Pong
A; Elawn, R.M.; Broonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Pong
A; Fitle: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
A;Reference number: 146259; MUD:96025778; PMID:7592597
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                                                                                                                                                                                                                                                                                                                                                                                                                                               F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
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A;Molecule type: mRNA
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TDSQLRWEYCEIPSCESS 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 80.6% Matches 208; Conservative
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apolipoprotein(a) - western Buropean hedgehog (fragment)
C;Species: Brinaceus europaeus (western Buropean hedgehog)
C;Species: Liacott-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18518
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.B.; Wade, D.P.; Byrne, C.D.; Fong, J.Bol., Chem. 270, 24004-24009, 1995
J;Biol. Chem. 270, 24004-24009, 1995
A;Fitle: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprote A;Reference number: 146259; MUID:96025778; PMID:7592597
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C;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, consent apolipoprotein(a).
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A;Cross-references: UNIEROT:Q28398; UNIPARC:UPI000008785C; EMBL:U33170; NID:g1046358; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 GFIPSKFPSKALKANYCRNPDGEPRPWCPTWDRNKRWEYCDIPRCTTPPPPSGFTYQCLM
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                                                                                                                                                                                                                                                                           GYI PSKFPUKULKKNY CRNPDRELRPWCFTTDPNKRWELCDI PRCTTPPPSSGPTYQCLK
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                                                                                                                                                                                                                                               DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENPPCKNLDENYCRNPDGKRAPWCHT
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                                                                                                                         1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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                                                               Gaps
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Length 810;
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                                                            Indela
   Score 1237; DB 2;
Pred. No. 8.4e-83;
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55.0%; Pred. No. 2.7e-56;
rative 36; Mismatches 70;
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A,Molecule type: mRNA
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                                                            26; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-31, "HK', 34-77, "N', 79-292, "V', 294-299, "M', 301-316, 'A', 318-335, 'K', 337-386,')
A; Cross-references: UNIPARC: UP1000015624E; EMBL: X16323; NID: 932081; PIDN: CAA34387.1; PID:
A; Experimental source: liver
A; Note: the authors translated the codon CAG for residue 727 as Glu
A; Note: part of this sequence, including the amino end of both the alpha and beta chains, A; Note: part of this sequence, including the amino end of both the alpha and beta chains, Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth factor A; Reference number: 159214; MUID: 93087511; PMID: 1280830
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-288, 'ET' <HAR>
A,Cross-references: UNIPARC:UPI0000073BF9; GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:c
R,Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Bur. J. Blocchem. 197, 15-22, 1991
A,Fitele: An alternatively processed mRNA generated from human hepatocyte growth factor ge
A,Reference number: S15443; MUID:91200041; PMID:1826653
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C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle; pyrc
C; Keywords: alternative spliting; glycoprotein; growth factor; heterodimer; kringle; pyrc
F; 1.31.Domain: signal sequence #status predicted <SIGS
F; 32-494,495-728 Product: hepatocyte growth factor #status experimental <MAT>
F; 32-494,Domain: alpha chain #status experimental <ACH>
F; 32-494,Domain: kringle homology <RR3>
F; 311-288 Domain: kringle homology <RR3>
F; 395-383 Domain: kringle homology <RR3>
F; 391-469,Domain: kringle homology <RR4>
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F;32/Modified site: pyrrolidone carboxyllic acid (Gln) (in mature form) #status experiment
F;294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;487-604/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',54
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',54
A;Cross-references: UNIPARC:UPI0000172B9A; UNIPARC:UPI0000172B9BC;
B;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashin Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: 806794; MUID:90066676; PMID:2531289
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A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 330/1; 424/2; 469/1; 48;
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
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A;Molecule type: mRNA
A;Molecule type: DID:
Cross-references: UNIPARC:UPI0000073BF9; EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:
R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
A;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
A;Title: Tumor cytocoxic factor/hepatcoyte growth factor from human fibroblasts: cloning
A;Reference number: I52253; MUID:92062058; PMID:1835383
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A;Cross-references: UNIPARC:UP100000353AB; GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:ç
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
7. Cell Biol. 111, 2097-22108, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasiveness
A;Reference number: A37796; MUID:91035621; PMID:2146276
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A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fact A;Reference number: A33512; MUID:89392017; PMID:2528952
                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
Date: 17-Aug-1992 #text change 09-Jul-2004
Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text change 09-Jul-2004
Accession: UH0579; UU0333; Ā41140; B3677; A36677; A33512; A39006; PH0114; A37796; S06
Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
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A, Residues: 1-728 <NBID:
A, Residues: 1-728 <NBID:
A, STROSS - 1-728 <NBID:
A, CTOSS - references: UNIPARC: UPI00000092B; GB: M73239; NID: G337935; PIDN: AAA64239.1; PID: R; Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M. Biochem. Blochya. Res. Commun. 172, 321-327, 1990
A; Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor.
A; Reference number: A36677; MUID: 91025062; PMID: 2145836
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A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy A;Reference number: A39006; MUID:91110540; PMID:1824873
A;Accession: A39006
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Residues: 1-728 <SE3>
Cross-references: UNIPARC:UPI000000092B; GB:M60718; NID:9184031; PIDN:AAA52648.1; PID:
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A, Cross references: UNPPARCIPT000017897
A, Cross references: UNPARCIPT000017897
R; Weidner, K.M.; Arakaki, N.; Harbmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A, Title: Evidence for the identity of human scatter factor and human hepatocyte growth A, Reference number: A41140; MUID:91334393; PMID:1831266
A, Accession: A41140
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A,Residues: 1-728 <SEK>
A,Residues: 1-728 <SEK>
A,Cross-references: UNIPARC: UNIPARC: UPI00000D92B; DDBJ: D90318
A,Cross-references: UNIPAT: D14210; UNIPARC: UPI00000D92B; DDBJ: D90318
A,Note: the authors translated the codon GAA for residue 662 as Gly
B,Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A,Description: Organization of the human hepatocyte growth factor-encoding gene.
A,Reference number: JU0333
A,Accession: JU0333
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K;Seki, T.; Haqiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A;Title: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JH0579; MUID:91340155; PMID:1831432
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Residues: 32-43;53-58 <YOS>
;Cross-references: UNIPARC:UP10000172B98; UNIPARC:UP10000172B99
                                                                                                                                                                                                         hepatocyte growth factor precursor [validated] - human
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A;Residues: 1-728 <MIY>
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Residues: 1-161,167-728 <SE4>
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Residues: 1-161,167-728 <RUB>
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Accession: B36677

Accession: A36677

Molecule type: DNA

Score 797; DB 1; Length 728; Pred. No. 9.4e-51;

51.8%;

Query Match Best Local Similarity

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Best Local Similarity 50.09
Matches 130; Conservative
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C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolc
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolc
C; Kayvords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F; 1-37 Domain: signal sequence #status predicted <&IGS
F; 56-495/Domain: hepatocyte growth factor #status predicted <&IGS
F; 56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F; 12-289/Domain: kringle homology <KR2>
F; 36-495/Domain: kringle homology <KR2>
F; 36-496/Domain: kringle homology <KR2>
F; 36-496/Domain: kringle homology <KR3>
F; 39-470/Domain: kringle homology <KR3>
F; 496-719/Domain: kringle homology <KR3>
F; 406-719/Domain: kring
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-728 cTAS
A; Molecule type: Type cTAS
A; Molecule type: Type cTAS
A; Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
A; Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
Biur. J: Biochem. 193, 735-381, 1990
A; Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dux
A; Reference number: S13211; MUID:91031482; PMID:2146117
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C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303
                                                                                                                                                                                                                                                                           GYIPSKFPNKULKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRC--TTPPPSSGP--TY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENPPCKNLDENYCRNPDGKRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 728;
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    81;
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 WCHTTNSQVRWEYC-KIPSCDSS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatocyte growth factor precursor - rat
    42;
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Best Local Similarity 49.8%
Matches 132; Conservative
    Conservative
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A;Molecule type: mRNA
A;Residues: 1-728 <OKA>
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134;
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    Matches
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61

YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND

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A; Note: does not have proteinage activity
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C; Keywords: duplication; glyooprotein; growth factor; heterodimer; kringle
C; Keywords: duplication; glyooprotein; growth factor alpha chain #status predicted <AMI>
C; 142-477, 478-709/Product: hepatocyte growth factor alpha chain #status predicted <AMI>
C; 1515-193/Domain: heringle homology <ARI>
C; 189-367/Domain: kringle homology <ARI>
C; 189-367/Domain: kringle homology <ARI>
C; 187-453/Domain: kringle homology <ARI>
C; 187-453/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
C; 187-181, 201, 322, 379, 550, 657, 666(Binding site: carbohydrate (Asn) (covalent) #status precipation of the covalent) #status precipation of the covalent is the covalent in the
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C;Accession: 151283
R;Nakamura, H.; Tsahiro, K.; Nakamura, T.; Shiokawa, K.
Mcch. - 13-131, 1995
A;Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus earl
A;Reference number: 151283; MUID:95267690; PMID:7748783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPARC:UP10000PDFB6; GB:S77422; NID:9998932; PIDN:AAB34354.1; PID:cA;Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleotic C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
KGIGENYRGNVAVITVSGHTCQHWSAQIPHTHERIPENFPCKNLDENYCRNPDGKRAPWCH 239
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                                                                                                                                                                                                                                            185 RGCPWCPTSNPEVRYEVCDIPQCSEVECMTCNGESYRGPMDHTESGKTCQRWDQQTPHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apatocyte growth factor precursor - clawed frog
Alternate names: hepapoietin A; scatter factor
iSpecies: Xenopus sp. (clawed frog)
blate: 13-8ep-1996 #sequence_revision 13-8ep-1996 #text_change 09-May-2004
incompanion: Telest
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                                                                                                                                                                                                                                                                                                                                                                                                      GYI PSKFPNKULKKNYCRNPDRELRPWCFTTDPNKRWELCDI PRCT-----TPPPSSGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPWCFTTDPNIRVGYCSQIPKCDVS 387
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A; Residues: 1-716 A; Residues: 1-716 A; Complex: UNIPROT:P70521; UNIPARC:UPI00000E833C; EMEL:X95096; NID:g1669718; PII
C; Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C; Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C; Keywords: duplication; glycoprotein; growth factor; kringle
F;11/Domain: signal sequence #status predicted <SIG>F;32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <AGH>F;32-488,Domain: macrophage-stimulating protein 1 alpha chain #status predicted <AGH>F;110-186/Domain: kringle homology <RRII>
F;29-370/Domain: kringle homology <RRII>
F;39-457/Domain: kringle homology <RRII>
F;39-457/Domain: kringle homology <RRII>
                                                                                                                                                                                                                                            Albescription: stimulates mitosis of hepatocytes and other cells
Mydote: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/marcophage stimulating protein 1; kringle homolocyteywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyrckeywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyrckeywords: alternative splicing; glycoprotein; growth factor algo-
E;56-495,496-728/Product: hepatocyte growth factor algo-
R;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
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F129-207/Domain: kringle homology <RR2>
F120-289/Domain: kringle homology <RR2>
F130-384/Domain: kringle homology <RR3>
F130-470/Domain: kringle homology <RR4>
F130-470/Domain: kringle homology <RR4>
F130-470/Domain: kringle homology <RR4>
F130-470/Domain: kringle homology <RR4>
F133-470/Domain: kringle homology <RR4>
F133-480-119/Domain: kringle homology <RR4>
F133-470/Domain: kringle homology <RR4>
F133-470/Domain: hepatocyte growth factor beta chain #status predicted
F133/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F125,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Affitle: Molecular cloning of rat macrophage-stimulating protein and its involvement in A; Reference number: UC5061; MUID:97011126; PMID:8858136
                                                                                                                   A;Cross-references: UNIPARC:UP100000006DC; EMBL:X81630; NID:g673451; PIDN:CAA57286.1; C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
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C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 EGGPWCFISNPEVRYEVCDIPQCSEVECMTCNGESYRGPMDHTESGKTCQRWDQTPHRH
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49.4%; Pred. No. 3.2e-49;
ive 40; Mismatches 84;
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4°
Matches 131; Conservative
                                                                                 A, Residues: 1-30 <RES>
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A;Molecule type: protein
A;Molecule type: protein
A;Cross-references: X'.184-188,'XX',194,'XX',197;357-364,'XX',367;375-377,'E',379,'
A;Cross-references: UNIPARC:UP10000172BA2;
R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
B;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
A;Lile: Biophya: Acta 1216, 229-303, 1993
A;Tile: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth A;Reference number: 843416; MUID:94060105; PMID:8241272
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Diol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Reference number: 149758; MUID:95122532; PMID:7822318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-728 <SAG3.
A;Cross-references: UNIPROT:Q08048; UNIPARC:UPI0000006E4; GB:D10212; NID:g220435; PIDN:
A;Experimental source: fibroblast, COS-1 cell
A;Note: submitted to JIPID, May 1993
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A;Title: Purification and characterization of biologically active scatter factor from
A;Reference number: S17173; MUID:91354223; PMID:1831975
                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: JC2117; PC2064; Ā60185; 543416; S45521; S17173; S10966; 148758; JU0231
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Biophys. Res. Commun. 199, 772-779; 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as A;Reference number: JC2117; MUID:94183257; PMID:8135822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 496-504 <SA2>
A; Residues: 496-504 <SA2>
A; Cross-references: UNIPARC: UPI0000172BA1
R; Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
A; Title: Purified scatter factor stimulates epithelial and vascular endothelial cell
A; Reference number: A60185; MUID: 90377927; PMID: 2144630
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A,Molecule type: protein
A,Residues: 496-570, XX, 509-512, LV, 514-516, XX, 518-519 <NAT>
A,Cross-references: UNIPARC:UP10000172BA8
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A;Status: preliminary
A;Molecule type: mmary
A;Residues: 1-563, "H' 565-728 < LL2>
A;Cross-references: UNIPARC:UPI0000172BA6; EMBL:X72307
R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Hepatocytes and scatter factor.
A,Reference number: S10966; MUID:90326152; PMID:2142751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPARC:UPI0000006E4; EMBL:X72307
                                                                                                                                                                                                                                                                                                                                 N, Alternate names: hepapoletin A; scatter factor
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R;Lu, Y.
submitted to the EMBL Data Library, May 1993
A;Reference number: S45521
                                                                                                                                                                                                                                                                                               hepatocyte growth factor precursor - mouse
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A;Residues: 496-517,'T',519 <COF>
A;Cross-references: UNIPARC:UP10000172BA7
    TINSQVRWEYC-KIPSCDSS 258
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TTDPNIRIGHCSQIKKCQAS 370
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Molecule type: mRNA
Residues: 1-728 <LIU>
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184

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macrophage-stimulating protein 1 precursor - mouse
N;Alternate names: hepatocyte growth factor-like protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul.1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A40332; B40332
R;Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
B;Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor
A;Reference number: A40332; MUID:92002017; PMID:1832957
                                                                                                                                                                                                                                                                                                                               Accession: A40332
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A; Reaidues: 1-411 <STR>
A; Cross-references: UNIPROT:Q90978; UNIPARC:UPI0000175C78; GB:S77480; NID:g998675; PID:g
C; Superfamanily: hepatocyre growth factor/macrophage stimulating protein 1; kringle homolo F; 124-197/Domain: kringle homology <KRG>
F; 202-279/Domain: kringle homology <KR2>
F; 205-374/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: I51285
R; Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
Bevelopment 121, 813-824, 1995
A; Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin
A; Reference number: I51285; MUID:95237013; PMID:7720585
P;489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>P;489-709/Domain: trypsin homology <TRY>F;72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                  164 PRGPWCYTTNRSVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDLQHPHSH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 PFHPEKFPDKALKONYCRNPDASERPWCYTTDPNVEREFCDLFSCGPNLPPTTKGSKSQQ 283
                                                                                                                                                                                                                                                                                                                         62 PQGPWCYTTDPEKRYDYCDILECEEE-CMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GYIPSKFPNKNLKKNYCRNPDRBLRPWCFTTDPNKRWBLCDIPRC--TTPPPSSGPTYQ- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----CLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 RNKVKASNCFRGKGEDYRGTTNTTSAGVPCORWDAONPHOHRFVPEKYACKDLRENFCRN 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heparocyte growth factor/scatter factor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                   2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND
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                                                                                                              DB 1;
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49.0%; Score 754.5; DB 2;
Best Local Similarity 50.2%; Pred. No. 6.7e-48;
Matches 132; Conservative 31; Mismatches 89;
                                                                                                        Query Match
Best Local Similarity 48.5%; Pred. No. 1.5e-48;
Matches 132; Conservative 36; Mismatches 89
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A;Molecule type: mRNA
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;Molecule type: DNA
;Residues: 1-716 <DEG>
;Cross-references: UNIFROT:P26928; UNIPARC:UP100000402E; GB:M74180; NID:g193831; PIDN:
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;Residues: 1-18,'P',20-716 <DEG2>
;Cross-references: UNIPARC:UPI0000027E40; GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g
                                                                                                                                                                                                                                                                                                                                                                              Aintrons: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47(
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C;Keywords: duplication; glycoprotein; growth factor; kringle
F:1-31/Domain: signal sequence #status predicted <SIG>
F:19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F:19-483/Domain: alpha chain #status experimental <ACH>
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NyAlternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C;Species: Homo sapiens (man)
C;Species: Jour-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Baton, D.L.; Chen, E.Y.; Fless, G.M.; Scan, Nature 330, 132-137, 1987
A;Title: CDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A;Reference number: S00657; WUID:88039109; PMID:3670400
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    SSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 YVRICIMDNGVSYRGIVARTAGGLPCQAWSRRFPNDHKYTPT--PKNGLEENFCRNPDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 PROPEKFLDXDLXONYCRNPDGSERPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;110-186/Domain: Kringle homology <KR1>
F;191-268/Domain: Kringle homology <KR2>
F;292-370/Domain: Kringle homology <KR3>
F;292-370/Domain: Kringle homology <KR4>
F;379-457/Domain: kringle homology <KR4>
F;379-450/Domain: kringle homology <KR4>
F;489-711/Domain: trypsin homology <TRY>
F;489-713,305,620/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDGKRAPWCHTTNSQVRWEYC-KIPSC 255
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completed: August 29, 2006, 14:01:59
                                               01/Domain:
                                                                                   F;1738-1815/Domain:
                                                                                                                       F;1852-1929/Domain:
                                                                                                                                                       F;1966-2043/Domain:
F;2080-2157/Domain:
                                                                                                                                                                                                                                       F;2194-2271/Domain:
                                                                                                                                                                                                                                                                                                                  F;2422-2499/Domain:
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F;2764-2841/Domain:
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                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 20-21, 'P', 23-34;177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200;292-314, 'W', 316-31
A; Residues: 20-21, 'P', 23-34;177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200;292-314, 'W', 316-31
A; Cross-references: UNIPARC: UP10000172BB0; UNIPARC: UP10000172BB2;
B; Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.; Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.; Mriller, Sci. W.S.A. 90, 1369-1373, 1993
A; Title: S. Control regions of the apolipoprotein(a) gene and members of the related pla A; Reference number: A47277; MUID:93165698; PMID:7679504
A; Residues: preliminary; translation not shown; translated from GB/EMBL/DDBJ
A; Residues: 1-16 cRES>
A;Residues: 1-4548 <MCL>
A;Residues: 1-4548 <MCL>
A;Cross-references: UNIPROT:P08519; UNIPARC:UP1000013C499; GB:X06290; EMBL:X06696; NID:9
A;Cross-references: UNIPROT:P08519; UNIPARC:UP1000013C499; GB:X06290; EMBL:X06696; NID:9
A;Caco. D.L.; Fless, G.M.; Kohr, W.J.; Mclean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3234
B;Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to A;Reference number: A28017; MUID:87204109; PMID:3472206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI0000062A8; GB:L07899; NID:g967973; PID:g967974
R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacco
Proc. Natl. Acad. Sci. US.A. 98; 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipopr A;Reference number: A47233; MUID:93087573; PMID:1454851
A;Accession: I60906
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-16 <-RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 31, 3113-3118, 1992

A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated windefile: Multiple members of the plasminogen-apolipoprotein(a) gene family associated windefile: Multiple member: 152415; MUID: 92207924; PMID: 1554698

A;Reference: 152415

A;Rolecule type: DNA

A;Residues: 1-16 < RE3>

A;Cross-references: UNIPARC: UPI00000662A8; GB:M86877; NID: G178780; PIDN: AAB49909:1; PID: A;Note: apo(a) gene 1 (nomenclature of reference 152415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UP10000062A8; GB:M90078; NID:g178786; PIDN:AAA35547.1; PID
A;Note: apo(a) gene 1 (nomenclature of reference I52415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPARC:UP100000062A8; GB:M90079; NID:g178784; PIDN:AAA35546.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPARC: UPI0000062A8; GB: M86878; NID: 9178782; PIDN: AAA51749.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:120699; OMIM:152200
A;Map position: 6q26-6q27
A;Note reveral genes closely linked on chromosome 6 are identical in the first coding rs of kringle repeats
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Reywords: hydrolase, kringle binding; lipoprotein; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-4549/Product: apolipoprotein(a) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ: Molecule type: DNA
Residues: 1-16 <RE5>
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A;Molecule type: DNA
A;Residues: 1-16 <RE4>
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F;142-219/Domain: kringle homology «KR2»
F;256-333/Domain: kringle homology «KR2»
F;370-447/Domain: kringle homology «KR4»
F;484-561/Domain: kringle homology «KR6»
F;598-675/Domain: kringle homology «KR6»
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3898 RGDGQSYRGTLSTTTTGRTCQSWSSMTPHWHRRIPLYYPNAGLTRNYCRNPDAEIRPWCY 3957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4018 YRGISSTTVTGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPWCYITDPCV 4077
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                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 YRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHTTNSQV
                                                                                                                                                                                                                                                                                                                                                                                                                3 LSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3958 IMDPSVRWEYCNLTRCPVTESSVLTTPTVAPVPSTEAPSEQAPPEKSPVVQDCYHGDGRS
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                             Length 4548;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                          Query Match
48.6%; Score 749; DB 1; L
Best Local Similarity 41.2%; Pred. No. 1.8e-46;
Matches 129; Conservative 45; Mismatches 81;
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

Run on:

August 29, 2006, 13:51:34; Search time 199 Seconds (without alignments) 597.368 Million cell updates/sec

Title: Perfect score:

US-09-502-176-2 1540 1 VYLSECKTGNGKNYRGTMSK.....TNSQVRWEYCKIPSCDSSFV 260 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 segs, 457216429 residues Searched:

Total number of hits satisfying chosen parameters:

2589679

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_8:* 1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp2000s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* geneseqp2005s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

## SUMMARIES

Description	Aab26486 Deqlycosy	Aau01209 Human Ang	Adk40316 C-termina	Adk40314 N-termina		•	Ø	표	Aaw07581 N-Termina	Aaw94038 Human and	Human	Adq47024 Human and	Human		Aed64669 Human ang	Aay70255 Human and		Aay79226 Angiogene	-	_	Aab16450 Human and	Aam48894 Human ang	Adg47063 Human kri
													-	/	/	/							
ΩI	AAB26486	AAU01209	ADK40316	ADK40314	AAG79748	AAY02109	AAY02102	AAR83961	AAW07581	AAW94038	AAM50518	ADG47024	ADM11543	AED08938	AED64669	AAY70255	AAY02106	AAY79226	AAY79225	AAW07579	AAB16450	AAM48894	ADG47063
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Length DB	260	260	869	869	260	268	285	339	339	339	339	333	339	339	339	363	364	374	375	378	378	378	378
Query Match	100.0	100.0	8.66	8.66/	99.7	7.66	7.66	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	99.7	7.66	99.7	99.7	99.7	7.66	99.7
Score	1540	.1540	1537	1537	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535
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Aed08977 Human kri Aav02105 A multifu		Ada08454 Mammalian	Adp67426 A61 anti-	Ada08455 Mammalian	Adp67427 A61 anti-	Aay79224 Angiogene	Aay02093 A multifu	Aay02099 A multifu	Aay02095 A multifu	Aay02096 A multifu	Aaw95051 Amino aci	Aay02112 A multifu	Abu64288 Human ang	Aag79749 Human pla	Abb75942 Endotheli	Aay02100 A multifu	Abb75944 Angiotens	Abb75943 Angiotens	Adg82532 Prolactin	Abm83810 Human dia
AED08977 AAY02105	AAY02101	ADA08454	ADP67426	ADA08455	ADP67427	AAY79224	AAY02093	AAY02099	AAY02095	AAY02096	AAW95051	AAY02112	ABU64288	AAG79749	ABB75942	AAY02100	ABB75944	ABB75943	ADG82532	ABM83810
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99.7	99.7	7.66	7.66	7.66	99.7	7.66	99.7	7.66	7.66	7.66	99.7	99.7	99.7	99.7	7.66	99.7	99.7	99.7	99.7	99.7
1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535	1535
2.5	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAB26486 standard; protein; 260 AA RESULT 1

AAB26486;

Deglycosylated kringle 1-5 region protein.

(first entry)

16-JAN-2001

Deglycosylated; kringle; angiogenesis; human.

Homo sapiens

WO200047729-A1.

17-AUG-2000.

10-FEB-2000; 2000WO-US003482. 

10-FEB-1999; 99US-0119562P. 37-APR-1999; 99US-0128062P. 07-APR-1999;

(ENTR-) ENTREMED INC. (CHIL-) CHILDRENS MEDICAL CENT.

Pirie-Shepherd S, Folkman MJ, Liang H,

ÿ Sim

Macdonald NJ,

WPI; 2000-579032/54. N-PSDB; AAA94906.

Novel composition comprising deglycosylated fragments of kringle 1-5 regions of plasminogen linked to the glycosylated form, useful for inhibiting angiogenesis.

Claim 7; Fig 1; 42pp; English.

The present sequence is deglycosylated kringle 1-5 region protein. Deglycosylated kringle 1-5 region protein has increased antiangiogenic activity as compared to glycosylated kringle 1-5 region protein. The deglycosylated kringle 1-5 region protein was isolated from human plasminogen by affinity chromatography

Sequence 260 AA;

Query Match

100.0%; Score 1540; DB 3; Length 260;

ocular angiogenic diseases, Osler-Webber

syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma and wound granulation. As a centrifugation technique is not employed in the process, damage to the cells with concomitant release of undesirable biological materials such as cytochromes, pigments, enzymes, chemicals and other undesirable purification of proteins is greater than that obtained from prior art methods. Active Angiostatin can be stored in buffers for extended periods of time, in vials or other containers, either in solution which may be liquid or frozen, or lyophilised

886666666666688888

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Gaps ö

Indels

100.0%; Score 1540; DB 4; 100.0%; Pred. No. 1.1e-90; ive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 260; Conservative

Sequence 260 AA;

Length 260;

120 120 180

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121 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180

121 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK

61 DPQGPWCYTTDPEKRYDYCDILECEBECWHCSGENYDGKISKTMSGLECQAWDSQSPHAH

1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH

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VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN

181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240

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                                                      1 VYLSECKTGNGKNYRGTMSKTKNGITCQK#SSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                           DPQGPWCYTTDPEKRYDYCDILECZEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
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                                 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTS24RPRFSPATHPSEGLEENYCRNPDN
            Gaps
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             Indels
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Schrimsher JL, Shepard SR;
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  100.0%; Pred. No. 1.1e-90;
tive 0; Mismatches 0:
                                                                                                                                                                                                                                                                                AAU01209 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                              Human Angiostatin (hASv3) protein.
                                                                                                                                                                                                                    241 TNSQVRWEYCKIPSCDSSPV 260
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Cocal Similarity 100.
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, Mistry FR,
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New albumin fusion protein comprising an angiogenesis inhibiting peptide
                                                                                                                                   cytostatic; vaccine; albumin fusion protein;
angiogenesis inhibiting peptide; anglogenesis-dependent tumor; cancer;
collagen.
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                                                                                                                                                                                                                                                                                                                     Hauser
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                                                                                                                                                                                                                                                                                                                     Hay
                                                                                                                          C-terminal albumin-angiostatin fusion protein
                                                                                                                                                                                                                                                                                                                    Sleep D,
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TNSQVRWEYCKIPSCDSSPV 260
             TNSQVRWEYCKIPSCDSSPV 260
                                                                  ADK40316 standard; protein; 869
                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS BEHRING GMBH.
(DELZ ) DELTA BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                   Kisker O,
                                                                                                                                                                                                                                                                      07-FEB-2002; 2002US-0355547P.
                                                                                                                                                                                                                                                   07-FEB-2003; 2003WO-IB000433
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                  Celik I,
                                                                                                                                                                                                                                                                                                                                      WPI; 2003-731479/69
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                                                                                                                                                                                  sapiens.
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241
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                                                                                   ADK40316;
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                                              RESULT 3
                                                        ADK40316
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The present sequence representing Angiostatin protein is given in an invention providing a method for recombinant production, recovery and purification of Angiostatin protein. Purification of recombinant Angiostatin comprises applying crude fermentation broth containing the protein to an expanded bed cation exchange column, eluting it, and applying the eluate to anion exchange column, repeating the process of eluting and applying, to hydroxyapatite column, hydrophobic column and membrane, in order, and collecting fluid passing through the membrane. Angiostatin is useful for treating angiosenesis mediated diseases, including solid tumours, leukaemia, tumour metastases, benign tumours,

Purifying recombinant angiostatin, involves applying fermented broth containing angiostatin to expanded bed cation exchange column, anion exchange column, hydroxyapatite column, hydrophobic column and a

2001-408277/43 N-PSDB; AAS04181 Example 1; Page 22; 49pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                         849
                                                               The invention relates to an albumin fusion protein comprising an angiogenesis inhibiting peptide and an albumin having an albumin activity, or their fragments or variants. The albumin fusion proteins, compositions, vaccines and methods are useful for treating angiogenesis-dependent tumor, e.g. cancer. This sequence represents an C-terminal albumin-angiostatin fusion protein.
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               variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
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and an albumin having an albumin activity, or their fragments or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; vaccine; albumin fusion protein; angiogenesis inhibiting peptide; angiogenesis-dependent tumor;
                                                                                                                                                                                        Score 1537; DB 7; Length 869;
Pred. No. 5.1e-90;
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                                      Disclosure, Fig 8; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TNSQVRWEYCKIPSCDSSPV 260
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(DELZ ) DELTA BIOTECHNOLOGY LTD.
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                                                                                                                                                                                                                  259; Conservative
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                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                              Sequence 869 AA;
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Synthetic.
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                                                                     The invention relates to an albumin fusion protein comprising an angiogenesis inhibiting peptide and an albumin having an albumin activity, or their fragments or variants. The albumin fusion proteins, compositions, vaccines and methods are useful for treating angiogenesis-dependent tumor, e.g. cancer. This sequence represents an N-terminal angiostatin-albumin fusion protein.
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and an albumin having an albumin activity, or their fragments or variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, plasminogen; angiostatin, neovascularisation; kringle domain;
cell proliferation; viral vector; replication-defective; cancer; tumour.
                                                                                                                                                                                                                                                                                                                                        85 DPQGPWCYTTDPEKKYDYCDILECEERCMHCSGENYDGKISKTWSGLECQAWDSQSPHAH
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                                                                                                                                                                                                     Score 1537; DB 7;
Pred. No. 5.1e-90;
1; Mismatches 0;
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                                           Disclosure; Fig 6; 136pp; English
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                                                                                                                                                                                                   99.84;
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the parent molecule. However, angiostatin containing all 4 kringle domains (K1-4) was found to be no more potent as an inhibitor of cell proliferation than an angiostatin only containing K1-3. Therefore, kringle 4 does not posses inhibitory activity. A fragment of the plasminogen coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity. The vector comprises a promoter capable of expressing human angiostatin operably linked to a structural gene encoding one or more domains of human angiostatin. The vector, which may be a replication-defective viral vector, is useful for inhibiting angiogenesis in a mammal, especially with cancer or a tumour This sequence represents kringle domains 1-3 of human plasminogen. A 38 kD N-terminal fragment of plasminogen is referred to as angiostatin and inhibits neovascularisation. Angiostatin contains 4 kringle domains of closure; Page 75-76; 83pp; English

Sequence 260 AA;

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                                                                                                             DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
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                            Gaps
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Length 260;
                            1; Indels
 99.7%; Score 1535; DB 6; 99.6%; Pred. No. 2.2e-90;
                            0; Mismatches
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               Best Local Simitality Matches 259; Conservative
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Best Local Similarity
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AAY02109 standard; protein; 268 AA (first entry) 16-JUL-1999 AAY02109; RESULT 6 AAY02109 

multifunctional protein of the invention.

Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production

Homo sapiens. Synthetic

08-APR-1999

WO9916889-A1

98WO-US020464 97US-0060609P 30-SEP-1998; 01-OCT-1997;

& CO G D (SEAR ) SEARLE

Caparon MH, Casperson GF, Gregory SA, Klein BK; Bolanowski MA,

WO9916889-A1 08-APR-1999.

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                                                                                                                                                         The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have antiangiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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                                                                      New multifunctional proteins useful for treating angiogenic-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.7%; Score 1535; DB 2;
99.6%; Pred. No. 2.3e-90;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A multifunctional protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY02102 standard; protein; 285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TINSQVRWEYCKIPSCDSSPV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TINSQVRWEYCKIPSCDSSPV 262
                                                                                                                        Claim 5; Page 104; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.6
Matches 259; Conservative
                                  WPI; 1999-255098/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 268 AA;
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Cao Y;

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The sequence represents a plasminogen fragment which is compared with the corresponding plasminogen fragments of monkey (AAR83961), pig (AAR83963) and cattle (AAR83964) origin (in Fig.2), as well as the with the first 339 amino acids of mouse angiostatin (AAR8396) (i.e. as's 98-436 of the complete 812 as plasminogen molecule AAR83959). Human angiostatin is a plasminogen fragment starting at as 97 or 99 of the complete plasminogen molecule. Angiostatin is an endothelial inhibitor, which reversibly inhibits proliferation of endothelial cells and thereby inhibits angiogenesis. It is useful in the treatment of a human or animal with angiogenic mediated disease e.g. arthritis, macular degeneration, diabetic retinopathy or cancer. Cells comprising angiostatin-coding sequences are useful for gene therapy of primary tumors
                                                                                                                                                                                                                                                                                                                                                                       Endothelial inhibitor Angiostatin – useful to treat angiogenic mediated disease esp. angiogenesis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 81-82; 108pp; English
                                                                                                                                                                                                                                                                              Oreilly MS, Folkman MJ, Sim KL,
                                                                                                                                                                                                                                CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                        94US-00248629.
94US-00326785.
                                                                                                              95WO-US005107.
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Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                           WPI; 1995-382990/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 339 AA;
                                                                                                              26-APR-1995;
                                                                                                                                                           26-APR-1994;
                                                                                                                                                                                   20-OCT-1994;
                   WO9529242-A1
                                                                02-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                              combinations of angiotetain, medicaterin, interferon, thrombospondin, interferon inducible protein and platelet factor 4, and have antiangiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, protette, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYIPSKPPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                            New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                             specification describes multifunctional proteins which comprise
                                                                                                                                                           Klein BK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%; Score 1535; DB 2; Length 285; 99.6%; Pred. No. 2.4e-90; ive 0; Mismatches 1; Indels
                                                                                                                                                           Gregory SA,
                                                                                                                                                           Casperson GF,
                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 97-98; 121pp; English
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                   98WO-US020464
                                                                97US-0060609P
                                                                                                                                                           Caparon MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
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Best Local Similarity 99.6
Matches 259; Conservative
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                                                                                                                                                                                                                             WPI; 1999-255098/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 285 AA;
                                                                                                            (SEAR ) SEARLE
                                                                                                                                                           Bolanowski MA,
                   30-SEP-1998;
                                                             01-OCT-1997;
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                                                                                                                                                                                   Mckearn JP;
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Length 339;

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120
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                                                                                                                                                                                                                                                                          121 GYIPSKEPNKNLKKAYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                                                                                              181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                           1 VYLSECKTGNGKNYRGTWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                     61 DPOGPWCYTTDPEKRYDYCDILECEEBCMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                    GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                   1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                          ö
                                          1; Indels
Score 1535; DB 2;
Pred. No. 2.8e-90;
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW07581 standard; protein; 339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      241 TNSQVRWEYCKIPSCDSSPV 260
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99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1997 (first entry)
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statin; plasminogen; endothelial inhibitor; therapeutic;

Homo sapiens therapy

man plasminogen peptide fragment.

RESULT 8 **AAR**83961

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us-09-502-176-2.rag

(first entry)

06-APR-1999

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Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy.
                                                                                                               Lin J;
                                                                                                                                                                                                                                                                                                               angiostatin which can be used in the invention
                                                                                                               Sim KL,
                                                                                                                                                                                Claim 59; Page 96-97; 203pp; English
                                                                                                               Cao Y,
                                                                                               CHIL-) CHILDRENS MEDICAL CENT.
                                                              95US-00429743.
96US-00605598.
96US-00612788.
                                              96WO-US005856
                                                                                                               Oreilly MS,
                                                                                                                               WPI; 1996-518662/51
                                                                                                                                                                                                                                                                                                                               Sequence 339 AA;
no sapiens.
                                               26-APR-1996;
                                                                              08-MAR-1996;
                                                                                                               Folkman MJ,
                              14-NOV-1996
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The invention relates to new methods and compositions for inhibiting fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from mutine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4 bRLS protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of mutine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy. The present sequence, which is the Netering and fragment of human angiostatin, is a specific aggregate

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240
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                                                                                                                                                                                                          61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                         121 GYIPSKFPNKALKKAYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 180
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                                                  Gaps
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Query Match
99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.8e-90;
Matches 259; Conservative 0; Mismatches 1; Indels
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Conservative
Best Local Sim.
Matches 259;
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                                       AAW94038 standard; protein; 339 AA.
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AAW94038

AAW94038 ID AAW9 XX AC AAW9

RESULT 10

ö The invention relates to inhibition of endothelial cell proliferation that comprises administering to an endothelial cell a plasminogen fragment having an amino acid sequence similar to the kringle 1-5 region of a plasminogen molecule. The plasminogen fragments can be derived from murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen fragments can be used for modulating angiogenesis and treating angiogenic—mediated disease e.g. solid tumours, for treating excessive or abnormal stimulation of endothelial cells, as a birth control agent; and in the treatment of diseases that have angiogenesis as a pathological consequence (see AAW94036 for details on the various diseases the plasminogen fragments can also be used for gene therapy. The products can be used for the production of antibodies and in detection and diagnosis. Sequences AAW94037 to W4441 represent angiostation Use of plasminogen fragments - having an amino acid sequence similar to the kringle 1-5 region, for inhibiting endothelial cell proliferation and 9 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60 fragments (protein derivatives of angiostatin or plasminogen, having an endothelial cell proliferation activity) of murine, human, Rhesus, porcine and bovine angiostatins respectively. The kringle regions that can be used in the invention are indicated in the features 1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN Gaps Plasminogen; kringle; endothelial; angiogenesis; tumour; leukaemia; rheumatoid arthritis; psoriasis; ocular angiogenic disease; ulcer; gene therapy; birth control; Crohn's disease; angiostatin. ö Length 339; 1; Indels Score 1535; DB 2; Pred. No. 2.8e-90; 0; Mismatches 1; Example 27; Fig 2A-C; 165pp; English. /note= "Kringle 1-2" 5. .84 'note= "Kringle 1-3" "Kringle 2-3" Location/Qualifiers /note= "Kringle 2" 178. .255 /note= "Kringle 3" note= "Kringle 1" (CHIL-) CHILDRENS MEDICAL CENT. 99.7%; 98WO-US010979 Human angiostatin fragment .255 .165 Folkman MJ, O'reilly MS; .165 'note= WPI; 1999-059809/05 Similarity Sequence 339 AA; angiogenesis. Ношо варіелв 29-MAY-1998; WO9854217-A1 30-MAY-1997; 03-DEC-1998. Query Match Peptide Peptide Peptide Peptide eptide Peptide 

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Best Local &
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                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing endothelial cell proliferation, useful for treating angiogenic -mediated diseases such as cancer, arthritis, comprises administering plasminogen fragment corresponding to kringle structures of plasminogen
         DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                               Angiostatin; plasminogen; human; angiogenesis; endothelial cell; cell proliferation; inhibitor; tumour; antipsoriatic; cytostatic; vasotropic; antitumour; dermatological; antinflammatory; antidiabetic; antixheumatic; antiathritic; ophthalmological; vulnerary; antiulcer; antibacterial; antiatherosclerotic; gynaecological; antipyretic;
                                                      181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENPPCKNLDENYCRNPDGKRAPWCHT
                                             GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                    DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                 GTGENYRGINVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                                                                                                                                                                                               5. .165
/label= Kringle-1-2
                                                                                                                                                                                                                                                                                                                                                                                                                     88. .255
/label= Kringle-2-3
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              . .255
|abel= Kringle-1-3
                                                                                                                                                                                       AAM50518 standard; protein; 339 AA
                                                                                                                      TNSQVRWEYCKIPSCDSSPV 260
                                                                                                                                 241 TNSOVRWEYCKIPSCDSSPV 260
                                                                                                                                                                                                                                                                                                                                                                                                   . .84
/label= Kringle-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        88. .165
/label= Kringle-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          178. .255
/label= Kringle-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cao Y;
                                                                                                                                                                                                                                                                                                                cardiant; contraceptive; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00866735.
98US-00066028.
99US-00309821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2001; 2001US-00788142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00338387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Folkman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'REILLY M S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OREI/) O'REILLY M S (FOLK/) FOLKMAN M J. (CAOY/) CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-647990/74.
                                                                                                                                                                                                                                                Human angiostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2001029246-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'reilly MS,
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-1998;
                                                                                                                                                                                                                             12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1997
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                                             121
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                                                                                                                      241
                                                                                                                                                                                                         AAM50518
                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                    RESULT 11
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The present sequence is that of human angiostatin. A claimed method of inhibiting endothelial cell proliferation involves administering a 'chibbiting endothelial sequence similar to the kringle 1-5 region of a plasminogen molecule. This includes a protein, termed angiostatin, defined by its ability to overcome the angiogenic conclusions at approximately amino acid 98. The PP is preferably derived from mouse, human, Rheaus monkey, pig or cattle (see Almios16.21). It is consed in methods and compositions for the treatment of an angiogenic mediated disease, including haemangioma, solid tumours, blood-borne tumours, leukaemia, metestaabis, telangicatesia, psoriasia, coronary collaterals, cerebral collaterals, programia, meterolarisation, collaterals, cerebral collaterals, arteriovenous malformations, ischaemic diabetic retinopathy, corneal graft rejection, retrolental fibroplasia, collaterals, cerebral collaterals, arterition, menstruation, placentration and cat scratch heamatopolesis, ovulation, menstruation, placentration and cat scratch fever. Angiostatin is also useful as birth control agent by preventing vascularisation required for rembryo implantation. The compositions are particularly useful for treating or repressing the growth of tumours. Cumours will prevent the growth or expansion of tumours will prevent or human or animal with prevascularised tumours will prevent or animal with prevascularised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYI PSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDI PRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GY I PSK P P N K K K K Y C R N P D R B L R P W C P T T D P N K R W B L C D I P R C T T P P P S G P T Y Q C L K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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o
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Pred. No. 2.8e-90;
0; Mismatches 1; Indels
Example 27; Fig 2A-C; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG47024 standard; protein; 339 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 99.6
259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2004
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DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to endothelial inhibitors called angiostatin which reversibly inhibit proliferation of endothelial cells. The invention is useful for diagnosing and treating angiogenic-mediated diseases such as cancer, arthritis, macular degeneration, diabetic retinopathy, psoriasis, scleroderma, Crohm's disease, wounds, peptic ulcer and fractures. The invention is also useful in gene therapy. The present sequence is the human angiostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPQGPWCYTTDPEKRYDYCDILECEEECWHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting endothelial cell proliferation, useful for treating cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRPSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis or diabetic retinopathy, comprises administering to an endothelial cell a proliferation-inhibiting amount of an angiostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1535; DB 7; Length 339;
Pred. No. 2.8e-90;
0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                       Sim KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 27; SEQ ID NO 3; 96pp; English.
Linflammatory; vulnerary; human
                                                                                                                                                                                                                                                                                                                                                       Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNSQVRWEYCKIPSCDSSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNSQVRWEYCKIPSCDSSPV
                                                                                                                                                                                                                99US-00309821.
99US-00335325.
99US-00338387.
                                                                                                                                 94US-00248629.
94US-00326785.
95US-00429743.
96US-00612788.
97US-00866735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.78;
                                                                                                         2002US-00127066
                                                                                                                                                                                                                                                         2001US-00788142
                                                                                                                                                                                                                                                                                                                                                       MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                      O'reilly
                                                                                                                                                                                                                                                                                                  O'REILLY M S
                                                                                                                                                                                                                                                                                     POLKMAN M J
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-540796/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                             CAO Y.
SIM K L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 339 AA;
                                                     US2003064926-A1
                                                                                                         22-APR-2002;
                                                                                                                                                                                                                                                          16-FEB-2001;
                          Homo sapiens
                                                                                                                                                            26-APR-1995;
08-MAR-1996;
30-MAY-1997;
                                                                                                                                   26-APR-1994;
20-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                       Folkman MJ,
                                                                                                                                                                                                     24-APR-1998
                                                                                                                                                                                                                                17-JUN-1999
                                                                                03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                              (CAOY/)
(SIMK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                    (FOLK/)
(OREI/)
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proliferation, comprising administrating intermedial cell a plasminogen fragment having an amino acid sequence similar to that of the plasminogen fragment having an amino acid sequence similar to that of the from murine, human, Rhesus, porcine or bovine plasminogen. Also included are the following: (1) a method of treating a mammal with an angiogenic-mediated disease; (2) a therapeutic composition for inhibiting endicated plasminogen fragment; and (3) a method of expressing a plasminogen the plasminogen fragment; and (3) a method of expressing a plasminogen fragment having an endothelial cell proliferation inhibiting activity. The method is useful for treating angiogenesis-dependent diseases including cancer. Angiogenesis-mediated diseases also include rheumatoid arthritis, psoriasis diabetic retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, observed angiogenesis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wew composition comprising an isolated nucleotide sequence that codes for a plasminogen fragment, useful for treating angiogenesis-dependent diseases including cancer, rheumatoid arthritis, psoriasis or macular degeneration.
                                                                                                                               endothelial cell proliferation; plasminogen; kringle 1-5; angiogenic-mediated disease; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; osler-Webber syndrome; myocardial angiogenesis; murine; human; Rhesus; porcine; bovine; angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of inhibiting endothelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (angiostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1535; DB 8;
Pred. No. 2.8e-90;
0; Mismatches 1;
                                                                                                 Human plasminogen fragment (angiostatin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 18; SEQ ID NO 3; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents human plasminogen fragment
ADM11543 standard; protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00866735.
97US-00989477.
98US-00066028.
99US-00309821.
                                                                                                                                                                                                                                                                                                                                                                                                           94US-00326785.
95US-00429743.
96US-00612788.
                                                                                                                                                                                                                                                                                                                                                           27-MAR-2003; 2003US-00401108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1999; 99US-00338387.
16-FEB-2001; 2001US-00788142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'reilly MS, Folkman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOLKMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-142673/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OREI/) O'REILLY M
                                                                                                                                                                                                                                                                                        US2004023877-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAO Y.
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-1998;
                                                                                                                                                                                                                                                                                                                           05-FEB-2004
                                                                   20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1997
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(CAOY/)
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Gaps ; 0 9 9 120 180 180 240 240 ö

RESULT 13

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us-09-502-176-2.rag

Sequence 339 AA;

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The present invention provides methods of inhibiting angiogenesis by increasing the concentration of kringle region fragments of plasminogen molecules in vivo. The invention is useful for inhibiting angiogenesis or seating an angiogenesis—mediated disease such as cancer. The invention has ouseful in gene therapy. The present sequence is human angiostatin in tragment. Angiostatin fragment is a derivative of plasminogen an endothelial cell prolliferation inhibiting activity. This
                                                                                                                                                                             240
                                                         120
                                                                         61 DPQCPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                  121 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                    121 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                         240
                            9
              1 VYLSECKTGNGKNYRGTMSKTKNGTTCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                         DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                           GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                         181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT
VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRRSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibition; plasminogen; angiogenesis disorder; antiangiogenic; cardiovascular disease; cancer; cytostatic; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting angiogenesis or treating an angiogenesis-mediated disease comprises administering to the human or the animal a kringle region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 18; SEQ ID NO 3; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment of a plasminogen molecule.
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                                                                                                                                                                                                                                       241 TNSQVRWEYCKIPSCDSSPV 260
                                                                                                                                                                                                                                                        241 TNSQVRWEYCKIPSCDSSPV 260
                                                                                                                                                                                                                                                                                                                                            AED08938 standard; protein; 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-00248629.
94US-00326785.
95US-0042743.
96US-00642778.
97US-00866735.
97US-00989477.
98US-00309813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00335614.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; angiostatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2005
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08-MAR-1996
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                                                                                                                                                                                120
                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                   121 GYIPSKFPNKALKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGGPTYQCLK 180
                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                      181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Therapeutic; anglogenesis inhibition; inflammation; antiinflammatory; ibrosis; diabetes; antidiabetic; chronic inflammation; edema; arthritis; antiarthritic; uveitis; ophthalmological; cancer; cytostatic; hyperglycemia; proteinuria; nephrotropic; anglostatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of a composition e.g. angiostatin and/or kringle 5 of plasminogen, tinhibit vascular leakage, inflammation and fibrosis in an animal having diabetes, chronic inflammation and arthritis.
                                                                                                             1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                              61 DPOGPWCYTTDPEKRYDYCDILECEBECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                 121 GYIPSKPPNKULKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                               Gaps
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               Length 339;
                                               Indels
               6
Score 1535; Db >,
No. 2.8e-90;
                             Pred. No. 2.86
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 3; 93pp; English.
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                                                                                                                                                                                                                                                                                                                                                      241 TNSQVRWEYCKIPSCDSSPV 260
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11-DEC-2003; 2003US-0528647P.
12-OCT-2004; 2004US-00963115.
            99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JAN-2006 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human angiostatin protein.
            Query Match
Best Local Similarity 99.6
Matches 259; Conservative
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ful in inhibiting vascular leakage, inflammation and fibrosis in an uveitis, macular edema, chronic inflammation, brain edema, arthritis, uveitis, macular edema, cancer, hyperglycemia, a kidney inflammatory disease, a disorder resulting in kidney fibrosis and/or a disorder of the kidney resulting in proteinuria. The present sequence is the human angiostatin protein. 88888888

Sequence 339

ö Gaps ö Query Match

99.7%; Score 1535; DB 9; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.8e-90;
Matches 259; Conservative 0; Mismatches 1; Indels

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Search completed: August 29, 2006, 13:56:10 Job time : 201 secs

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539.087 Million cell updates/sec
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/EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW-PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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                                                                                                                          1540
1 VYLSECKTGNGKNYRGTMSK......TNSQVRWEYCKIPSCDSSPV 260
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                                                                   August 29, 2006, 14:14:04 ; Search time 33 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-318-939-11
US-11-318-939-13
US-11-318-939-12
US-11-318-939-9
US-11-328-070-14
US-11-328-070-14
US-11-328-070-12
US-11-328-070-13
US-11-328-070-13
US-11-328-070-13
US-11-318-939-8
US-11-318-939-8
US-10-503-836-41
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                                                                                                                                                                                                  247503 segs, 68422524 residues
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Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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10:6
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9:7
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	ALIGNMENTS					
Sequence 16, Appl	US-11-264-243-16	7	1953	4.9	98.5	45
Sequence 22, Appl	US-11-071-796A-22	7	2556	6.7	102.5	44
Seguence 6, Appli	US-11-264-243-6	7	2556	6.8	104.5	43
Sequence 25, Appl	US-11-290-896-25	7	631	6.9	105.5	42
Sequence 40, Appl	US-11-290-896-40	7	429	6.9	105.5	41
Sequence 19, Appl	US-11-071-796A-19	7	685	6.9	106	40
Sequence 2, Appli	US-11-264-243-2	7	685	6.9	106	39
	US-11-178-724-20	7	685	6.9	106	38
Sequence 38, Appl	US-11-175-714-38	7	685	6.9	106	37
	US-11-175-714-36	7	685	6.9	106	36
Sequence 34, Appl	US-11-175-714-34	7	685	6.9	106	35
Sequence 32, Appl	US-11-175-714-32	7	685	6.9	106	34
Sequence 28, Appl	US-11-175-714-28	7	685	6.9	106	33
Sequence 2, Appli	US-11-175-714-2	7	685	6.9	106	32
Sequence 24, Appl	US-11-290-896-24	7	663	7.0	108	31
Sequence 12, Appl	US-11-330-353-12	-	138	8.7	134	30
Sequence 2, Appli	US-11-311-475-2	^	477	8.8	135	29
Sequence 2, Appli	US-11-264-088-2	7	477	8.8	135	28
Sequence 34, Appl	'US-11-183-218-34	7	431	8.8	135	27
Sequence 465, App	US-10-505-928-465	9	431	8.8	135	26

PEPTIDES

TYPE: PRT
ORGANISM: Artificial Sequence
PRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amio acid sequence of the
OTHER INFORMATION: N-terminal angiostatin (non glycosylated) - albumin fusion proteir
US-10-503-836-35

Query Match 99.8%; Score 1537; DB 6; Length 869; Best Local Similarity 99.6%; Pred. No. 2.3e-120; Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps

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180 145 GYIPSKEPDKKULKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 204 61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120 9 84 25 VYLSECKTGNGKNYRGTMSKTKNGTTCQKWSSTSPHRPRFSPATHPSEGLBENYCRNPDN 85 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH GYIPSKFPNKALKKAYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 1 VYLSECKTGNGKAYRGTMSKTKANGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 121 Š 셤 ò 셤 ò g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 258
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PRIOR APPLICATION NUMBER: US/09/500,397
PRIOR PILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
PRIOR PILING DATE: 2000-02-08
PRIOR FILING DATE: EARLIER PAPLICATION NUMBER: 08/710,305
PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
PRIOR FILING DATE: EARLIER PILING DATE: 1997-12-15
PRIOR FILING DATE: EARLIER PILING DATE: 1997-12-15
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 791
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APPLICANT: Rasamcelisolo, Michele
APPLICANT: Rasamcelisolo, Michele
APPLICANT: Hibaudeau, Karen
APPLICANT: Hibaudeau, Karen
APPLICANT: Huang, Xicai
APPLICANT: Huang, Xicai
APPLICANT: Beliveau, Richard
ITILE OF INVENTION: LONG LASTING ANTI-ANGIOGENIC PEPTIDES
FILE REPERENCE: 500662001401
CURRENT APPLICATION NUMBER: US/01/350,703
CURRENT FILING DATE: 2006-02-08
PRIOR APPLICATION NUMBER: US 09/623,543
PRIOR APPLICATION NUMBER: 05/0134,406
PRIOR PILING DATE: 2000-05-17
PRIOR PLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1090-05-17
PRIOR PLICATION NUMBER: 60/134,406
PRIOR PLICATION NUMBER: 60/134,406
PRIOR PLICATION NUMBER: 60/134,406
PRIOR PLICATION NUMBER: 60/154,406
PRIOR PLICATION NUMBER: 60/153,406
PRIOR PLICATION NUMBER: 60/153,406
PRIOR PLICATION NUMBER: 60/153,703
PRIOR PLICATION NUMBER: 60/153,706
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Pred. No. 3.1e-120;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-318-939-6
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LENGTH: 790
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYIPSK#PNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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                                                                                          205 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHQRTPENFPCKNLDENYCRNPDGKRAPWCHT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGENYRGNVAVTVSGHTCQHWSAQTPHTHQRTPENFPCKNLDENYCRNPDGKRAPWCHT 849
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Publication No. US20060099671A1
Publication No. US20060099671A1
Publication No. US20060099671A1
APPLICANT: Softering Garald
APPLICANT: Gately, Stephen T.
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION! METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
PILE REPERRICE: 4228-1-1-1
CURRENT APPLICATION NUMBER: US/11/318,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            610 VYLSECKTGNGKNYRGTWSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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C-terminal albumin angiostatin (non glycosylated)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Appl cation US/10503836

Publication No. U$20060122374A1

GENERAL INFORMATION:

APPLICANT: Mertimb. Peter

APPLICANT: Sleep, Darrell

APPLICANT: Sleep, Darrell

APPLICANT: Hauser, Hans-Peter

TIE OF INVENTION: ALBUNN FUSED ANTI-ANGIOGENESIS PEPTIDES

TIE OF INVENTION: ALBUNN FUSED ANTI-ANGIOGENESIS PEPTIDES

TIE REFERENCE: #27, 972 USA

CURRENT RILING DATE: 2004-08-06

PRIOR PILING DATE: 2003-02-07

PRIOR FILING DATE: 2003-02-07

PRIOR FILING DATE: 2003-02-07

PRIOR FILING DATE: 2002-02-07

NUMBER OF SEQ IN NOST: 21

SOUTHARE PETENCHING DATE: 2002-02-07

SOUTHARE PETENCHING DATE: 2002-02-07

SOUTHARE PETENCHING DATE: 2002-02-07

SOUTHARE PETENCHING DATE: 2002-02-07

SOUTHARE PETENCHING DATE: 2002-02-07
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                                                                                                                                                                             241 TNSQVRWEYCKIPSCDSSPV 260
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                                                                                                                                                                                                                                                          265 TNSOVRWEYCKIPSCDSSPV 284
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-503-836-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-503-836-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 37
LENGTH: 869
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Query Match 83.9%
Best Local Similarity 81.4%
Matches 210; Conservative
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APPLICANT: Soff, Gerald
APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Gately, Stephen T.
APPLICANT: Gately, Stephen T.
TALE OF INVENTION: WETHORS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN FILE OF INVERNION NUMBER: US/1318,939
CURRENT FILING DATE: 2005-12-2-3
PRIOR PLILING DATE: 2000-02-08
PRIOR PLLING DATE: EARLIER PELLIGH APPLICATION NUMBER: 08/710,305
PRIOR APPLICATION NUMBER: BARLIER PRILING DATE: 1996-09-17
PRIOR PLLING DATE: EARLIER FILING DATE: 1997-12-15
PRIOR PLLING DATE: EARLIER PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: PCT/US97/16539
PRIOR PLLING DATE: EARLIER PLLING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENT NOS: 17
SOFTWARE: PATENT NOS: 17
SOFTWARE: PATENT NOS: 17
LENGTH: 810
                                                                                                                                                                                                                               79 VYLSECKTGNGKNYRGT-SKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 137
                                                                                                                                                                                                                                                                                            DPQGPWCYTTDPEKRYDYCDILLECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                   198 GYIPSKFPNKALKKAYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGFTYQCLK 257
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                                                                                                                                                                                                                                                                                                                                                                                   GYIPSKRPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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                                                                                                            Query Match
98.7%; Score 1519.5; DB 7; Length 790;
Best Local Similarity 99.2%; Pred. No. 6e-119;
Matches 258; Conservative 0; Mismatches 1; Indels 1;
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                ; FRATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-350-703-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TNSQVRWBYCKIPSCDSSPV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 TNSQVRWEYCKIPSCDSSPV 337
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Publication No. US20060099671A1
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Macaca mulatta
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APPLICANT: Soff, Gerald
APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Twardowski, Przemysław
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-1-1.
CURRENT APPLICATION NUMBER: US/09/500,397
PRIOR PILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US/10/500,397
PRIOR PILING DATE: 2000-02-08
PRIOR PILING DATE: RAKLIER APPLICATION NUMBER: 08/710,305
PRIOR PLING DATE: RAKLIER FILING DATE: 1996-09-17
PRIOR PLING DATE: EARLIER FILING DATE: 1997-12-15
PRIOR PLING DATE: EARLIER FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1997-09-17
SOFTWARE: PARCHER PILING DATE: 1907-09-17
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GTGENYRGNVAVIVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
                                     278 GTGENYRGDVAVTVSGHTCHGWSAQTPHTHNRIPENFPCKNLDENYCRNPDGEKAPWCYT 337
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APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Taradowski, Przemyslaw
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-1-1-1
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; Pred. No. 5.6e-100;
23; Mismatches 25;
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Publication No. US20060099671A1
GENERAL INFORMATION:
                                                                                                                                       241 TNSQVRWEYCKIPSCDSSPV 260
                                                                                                                                                                                                       338 INSOVRWEYCKIPSCESSPV 357
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Publication No. US20060099671A1
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|TDSEVRWDYCKIPSCGSS 336
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81.4%;
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208; Conservative
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APPLICANT: Soff, Gerald
APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Gately, Przemyslaw
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REPERENCE: 4228-1-1-1
CURRENT APPLICATION NUMBER: US/11/318,939
CURRENT APPLICATION NUMBER: US/09/500,397
PRIOR FILING DATE: 2006-12-22
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 08/710,305
PRIOR PILING DATE: EARLIER PILING DATE: 1996-09-17
PRIOR PLING DATE: EARLIER PILING DATE: 1997-12-15
PRIOR PLING DATE: EARLIER PILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
PRIOR PILING DATE: EARLIER PILING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTH PILING DATE: 1997-09-17
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                                      PRIOR APPLICATION NUMBER: US/09/500,397
PRIOR PILLING DATE: 2000-02-08
PRIOR PILLING DATE: 2000-02-08
PRIOR PILLING DATE: 2000-02-08
PRIOR PILLING DATE: EARLIER PILLING DATE: 1996-09-17
PRIOR PILLING DATE: EARLIER PILLING DATE: 1997-12-15
PRIOR PILLING DATE: EARLIER PILLING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: EARLIER PELLING DATE: 1997-09-17
PRIOR PILLING DATE: EARLIER FILLING DATE: 1997-09-17
SOFTWARE: PATCHING DATE: 2.1
SOFTWARE: PATCHING DATE: 1207-09-17
SOFTWARE: PATCHING VET. 2.1
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Pred. No. 1.8e-98;
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80.8%; Pred. No. 6.9e-100;
iive 23; Mismatches 27;
CURRENT APPLICATION NUMBER: US/11/318,939
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Publication No. US20060099671A1
GENERAL INFORMATION:
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80.6%;
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Best Local Similarity 80.8
Matches 210; Conservative
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; ORGANISM: Mus musculus
US-11-318-939-12
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ORGANISM: Bos taurus
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Best Local Similarity
                     FILING DATE:
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APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-11-1
CURRENT APPLICATION NUMBER: US/09/500,397
PRIOR PLING DATE: 2000-02-08
PRIOR PLING DATE: EARLIER PELLING DATE: 1996-09-17
PRIOR APPLICATION NUMBER: EARLIER PELLING DATE: 1996-09-17
PRIOR APPLICATION NUMBER: EARLIER PELLING DATE: 1997-12-15
PRIOR PILING DATE: EARLIER FILING DATE: 1997-12-15
PRIOR PILING DATE: EARLIER FILING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SEQ ID NOS: 17
SEQ ID NOS: 17
SEQ ID NOS: 17
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Gaps
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28; Indels
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22; Mismatches
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Publication No. US20060099671A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TNSQVRWEYCKIPSCDSS 258
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Matches 201; Conservative
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Pred. No. 1.1e-58;

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Best Local Similarity 50.29
Matches 133; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-328-070-2
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US-10-505-928-547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                               Sequence 14, Application US/11328070

Publication No. US20060104964A1

GENERAL INFORMATION:

APPLICANT: JIANG, WENG

TITLE OF INVENTION: RECOMBINANT SEQUENCE, ITS PREPARATION AND USE

FILE REPERENCE: 3007-1017

CURRENT PELING DATE: 2006-01-10

FRIOR PELING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-04

PRIOR FILING DATE: 2001-05-04

PRIOR PILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 34

SSQ ID NO 14

LEAR SOFTWARE: PATCHIN VET. 2.1

STO ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13, Application US/11328070
; Publication No. US20060104964A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JIANG, WER G.
1TILE OF INVENTION: RECOMBINANT SEQUENCE, ITS PREPARATION AND USE
FILE REFERENCE: 3007-1017
; CURRENT APPLICATION NUMBER: US/11/328,070
; CURRENT APPLICATION NUMBER: PCT/GB01/01956
; PRIOR PILING DATE: 2000-05-04
; PRIOR PILING DATE: 2000-05-04
; PRIOR PILING DATE: 2000-05-04
; RICH APPLICATION NUMBER: QE 0010630.2
; RICH APPLICATION VUMBER: 2001-05-04
; SEQ ID NO 13
; AGENCIAL 482
; TYPE: PRIOR PILING DATE: 2000-05-04
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 338 TNSSVRWEFCKIPDCVSS 355
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Matches 133; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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306 TIECIQGQGEGYRGIANTIWNGIPCQRWDSQYPHKHDMTPENFKCKDLRENYCRNPDGSE 365
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                                                                                                             2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND
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; Sequence 2, Application US/11328070
; Publication No. US20060104964A1
; GENERAL INFORMATION:
    APPLICANT: JIANG, WER G.
    TITLE OF INVENTION: RECOMBINANT SEQUENCE, ITS PREPARATION AND USE
; TITLE OF INVENTION: RECOMBINANT SEQUENCE, ITS PREPARATION AND USE
; FILE REPERENCE: 3007-1017
; CURRENT APPLICATION NUMBER: US/11/328,070
; PRIOR PILING DATE: 2006-01-10
; PRIOR PELING DATE: 2001-05-04
; PRIOR PILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PATENTIN VEY: 2.1
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51.6%; Score 794; DB 7; Length 566;
Best Local Similarity 50.2%; Pred. No. 1.3e-58;
Matches 133; Conservative 41; Mismatches 81; Indels
                                                     81; Indels
                                                     Mismatches
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50.2%; Fi.
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SEQ ID NO 26
LENGTH: 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 562;
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APPLICANT: BAYES, DAVID
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
TITLE OF INVENTION: ERYTHROPOLETIN: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOLETIN
FILE REFERENCE: 0.04083-01-5083-002
CURRENT APPLICATION NUMBER: US/11/183,218
CURRENT APPLICATION NUMBER: US/11/183,218
CURRENT APPLICATION NUMBER: US 10/410,945
PRIOR FILING DATE: 2003-04-09
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PELING DATE: 2002-08-28
PRIOR PELING DATE: 2002-08-16
PRIOR PELING DATE: 2002-08-17
PRIOR PELING DATE: 2002-08-28
                                                                                                      et al.
Sequence 547, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICATION NO. US2006008853A1

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILLE REPERENCE: 28957/39179
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR PILING DATE: 2002-007
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
LENGTH: 562
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PDELICATION NUMBER: US 60/387,292
FILING DATE: 2002-06-07
APPLICATION NUMBER: US 60/344,692
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APPLICATION NUMBER: US 60/334,301
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Publication No. US20060088906A1
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GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T: DeFrees, Shawn
T: Zopf, David
T: Bayer, Robert
T: Hakes, David
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CRGANISM: Homo sapiens
US-10-505-928-547
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APPLICANT: Soff, Gerald
APPLICANT: Gately, Stephen T.
APPLICANT: Gately, Stephen T.
APPLICANT: Gately, Stephen T.
APPLICANT: Twardowski, Przemyslaw
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVERTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
FILE REFERENCE: 4228-1-1-1
CURRENT APPLICATION NUMBER: US/11/318,939
CURRENT PILLING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-09-17
PRIOR PILLING DATE: BARLIER FILING DATE: 1997-09-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/334,233
PRIOR FILING DATE: 2001-11-28
Remaining Prior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ 1D NOS: 75
SOFTWARE: PatentIn version 3.2
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20.1%; Score 309.5; DB 7; Length EBest Local Similarity 34.1%; Pred. No. 3.2e-18;
Matches 77; Conservative 23; Mismatches 103; Indels
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Publication No. US20060099671A1
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Best Local Similarity 48.5%;
Matches 47; Conservative 13
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US-11-318-939-8
                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-183-218-26
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Search completed: August 29, 2006, 14:17:35 Job time : 34 secs

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121 GYIPSKFPNKALKKAYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-415-012-2
US-10-735-577-8
US-10-735-872B-7
US-10-741-601-413
US-10-995-561-764
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US-09-788-142-3
US-09-335-325-3
US-10-131-241-3
US-10-131-241-3
US-10-401-108-3
US-110-874-3
US-110-874-3
US-10-10-874-3
US-10-292-418-11
US-09-873-676-1
US-10-131-241-42
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Maximum DB
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RESULT 1
US-10-131-241-61
is Sequence 6.1, Application US/10131241
is Sequence 6.1, Application US/10131241
is Publication No. US20030012792A1
is GENERAL INFORMATION:
is APPLICANT: Holaday, John W.
is APPLICANT: Fortier, Anne H.
is TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifere
is TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
is TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
is TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
is TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
is TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
is TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
is CURRENT FILING DATE: 1999-10-06
is PRIOR FILING DATE: 1999-10-06
is PRIOR FILING DATE: 1999-05-21
is PRIOR FILING DATE: 1999-05-22
is NUMBER OF SEQ ID NOS: 65
is SUFTWARE PatentIn Version 3.1
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100.0%; Pred. No. 2.3e-120;
ative 0; Mismatches 0;
US-10-449-609-7

US-10-515-012-8

US-09-967-386-1

US-10-304-287-1

US-10-304-287-1

US-10-304-287-1

US-10-778-42-1

US-10-778-42-1

US-10-753-646-1

US-10-753-646-1

US-10-753-646-1

US-10-753-646-1

US-10-753-646-1

US-10-503-910-17

US-11-108-621-4

US-11-108-459-8

US-11-108-621-4

US-10-503-910-10

US-10-503-910-10

US-10-503-910-10

US-10-103-656-2

US-10-103-656-2
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Best Local Similarity 100.
Matches 260; Conservative
   ORGANISM: Homo sapiens
  US-10-131-241-61
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  SEQ ID NO 61
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US-09-788-142-3
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                          | FULLICATION NO. USZUGAGOZASAI
| GENERAL INFORMATION:
| APPLICANT: NAYLOR, STUART
| APPLICANT: NAYLOR, STUART
| APPLICANT: KINCSMAN, SUSAN MARY
| APPLICANT: KINCSMAN, SUSAN MARY
| APPLICANT: BINLEY, KATIE
| TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
| TITLE REFERENCE: 674533-2039.1
| CURRENT APPLICATION NUMBER: US/10/810,262
| PRIOR PILING DATE: 2004-03-26
| PRIOR PLILING DATE: 2001-07-06
| PRIOR PLILING DATE: 1999-09-22
| PRIOR PLILING DATE: 1999-09-23
| PRIOR PLILING DATE: 1999-09-23
| PRIOR PLILING DATE: 1999-01-28
| PRIOR PLILING DATE: 1999-02-16
| NUMBER OF SEQ ID NOS: 34
| SEQ ID NO 11
| LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Folkman, M. Judah
O'Reilly, Michael
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
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Pred. No. 7.2e-120;
Sequence 11, Application US/10810262
Publication No. US20040234505A1
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Patent No. US20010029246A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM
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Best Local Similarity 99.6
Matches 259; Conservative
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US-10-810-262-11
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Sequence 3, Application US/09761120
Patent No. US20020037847A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoger
FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: US/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR PILING DATE: 1999-05-11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 08/866,735
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELLECOMPUNICATION: NUMBER: 05940-0129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
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STRANDEDNESS: <Unknown>
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Best Local Similarity 99.6
Matches 259; Conservative
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GYIPSKPPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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Patent No. US20020164717A1

GENERAL INFORMATION:

GENERAL INFORMATION:

Cao, Yihai

Cao, Yihai

TITLE OF INVENTION: Angiostatin Fragments and Method of Use

NUMBER OF ENQUENCES: 45

CORESPONDENCE 45

CORESPONDENCE ADDRESS:

ADDRESSER: Jone & Askew

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STRATE: Georgia

COUNTRY: U.S.
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                            Score 1535; DB 3; Length 339;
Pred. No. 8.2e-120;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: <Unknown>
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 17-Jun-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TNSQVRWEYCKIPSCDSSPV 260
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                                                                                                                                                                                              Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative
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                                                                                                                   type: PRT
CORGANISM: Homo sapiens
US-09-761-120-3
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Science 3. Application US/10131241
Publication No. US20030012792A1
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT:
FOLIAL OF INVENTION:
APPLICANTION:
GENERAL OF INVENTION:
GENERAL ABJ 70-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-22
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Pred. No. 8.2e-120;
0; Mismatches 1;
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Pred. No. 8.2e-120;
0; Mismatches 1;
                                                                                                                                                                                                                                                                          CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
LENGTH: 339 amino acide
TYPE: amino acid
STRANDEDNESS: cUnknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
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Best Local Similarity 99.6%;
Matches 259; Conservative (
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 99.6'
Matches 259; Conservative
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US-10-131-241-3
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181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT 240
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O'Reilly, Michael
ITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 339;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/401,108
FILING DATE: 27-Mar-2003
CLASSIFICATION: 435
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STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
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99.6%; Pred. No. 8.2e-120;
iive 0; Mismatches 1;
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APPLICATION NUMBER: US/08/866,735
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN, William L.
REGISTRATION NUMBER: 36,714
FILE REFERENCE: 05213-2151 (43170-252068)
CURRENT APPLICATION NUMBER: US/10/402,364
CURRENT FILING DATE: 2003-03-28
FRIOR APPLICATION NUMBER: US/09/761,120A
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 3
LENGTH: 339
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COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Publication No. US20040023877A1
GENERAL INFORMATION:
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Best Local Similarity 99.6
Matches 259; Conservative
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US-10-402-364-3
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Publication No. US20040002459A1
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoge
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     VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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Publication No. US20030064926A1

FORDERAL INFORMATION:

APPLICANT: O'Reilly, Michael S.

APPLICANT: Folkman, M. Judah

APPLICANT: Cao, Yihai

APPLICANT: APPLICANT: Application Fragments and Method of Use

TITLE OF INVENTION: Angiostatin Fragments and Method of Use

FILE REFERENCE: 05213-0612 43170-272529

CURRENT APPLICATION NUMBER: US/10/127,066

UNBER OF SEQ ID NOS: 45

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin version 3.1
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99.6%; Pred. No. 8.2e-120;
iive 0; Mismatches 1;
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Best Local Similarity 99.6
Matches 259; Conservative
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APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
CURRENT APPLICATION NUMBER: 10910/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR PLILING DATE: 1999-08-25
PRIOR PLILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
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                                                                                               1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
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Pred. No. 8.9e-120;
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Best Local Similarity 99.6%; Pred. No. 8.9e
Matches 259; Conservative 0; Mismatches
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Sequence 11. Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
     259; Conservative
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     Matches
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Publication No. US20050250694A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING SAME
TITLE OF INVENTION: FIRROSIS AND METHODS OF MAKING AND USING SAME
TITLE OF INVENTION: FOR TITLE OF 1004-12-13
FILE REFERENCE: 5820.656
CURRENT FILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/510,620
PRIOR APPLICATION NUMBER: 60/510,620
PRIOR PLILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 3
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DPQGPWCYTTDPEKRYDYCDILLECERECMHCSGENYDGKISKTWSGLECQAWDSQSPHAH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTJDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.7%; Score 1535; DB 4;
Best Local Similarity 99.6%; Pred. No. 8.2e-120;
Matches 259; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%; Score 1535; DB 6; 99.6%; Pred. No. 8.2e-120;
REFERENCE/DOCKET NUMBER: 05940-0129
                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: Angiostatin fragment SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                  TELECOMMUNICATION INFORMATION:
TELEPRAK: (404) 818-3700
TELEPRAK: (404) 818-3700
TELEPRAK: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acide
TYPE: amino acid
STRANDENESS: cUnknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SORREE:
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IMMEDIATE SOURCE:
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; ORGANISM: Homo sapiens
US-11-010-874-3
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Best Local Similarity
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APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer:
TITLE OF INVENTION: Compositions and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT PELINGN NUMBER: US 05/10/131,241
CURRENT FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR PRILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
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99.6%; Pred. No. 9.3e-120;
tive 0; Mismatches 1;
                                                                                                    ATORNEY AGENT INPORMATION:
NAME: Warren, William L.
REGISTATION UNDERR: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3709
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                    APPLICATION NUMBER: US/08/612,788 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: K1-4BKLS

CLONE: K1-4BKLS

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-131-241-42
Sequence 42. Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: curknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                              PRIOR APPLICATION DATA
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Matches 259; Conservative
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                                                                  GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas J.
APPLICANT: MacDonald, Nicholas J.
APPLICANT: Sim, Kim L.
TITLE CANT: Sim, Kim L.
TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use FILE REPERENCE: 05213-0378 (43170-259333)
CURRENT APPLICATION NUMBER: US/09/873,676
CURRENT FILING DATE: 2001-06-04
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin Version 3.1
SEQ ID NO : 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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APPLICANT: Folkman, M. Judah

Cao, Yihai

Cao, Yihai

Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45

CONTESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 1911 Peachtree Street, 37th Floor
CITY: Atlanta
CUNTRY: U.S.

ZIP: 330303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.7%; Score 1535; DB 3; Length 378; Best Local Similarity 99.6%; Pred. No. 9.3e-120; Matches 259; Conservative 0; Mismatches 1; Indels
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COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
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                         Sequence 1, Application US/09873676 Patent No. US20020077289A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-873-676-1
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US-09-873-676-1
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186 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT 245
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| Sequence 42, Application US/10127066
| Publication No. US2003006492641
| GENERAL INFORMATION:
| APPLICANT: O'Reilly, Michael S. APPLICANT: Folkman, M. Judah
| APPLICANT: Sim, Kim Lee
| TITLE OF INVENTION: Angiostatin Fragments and Method of Use
| TITLE OF INVENTION: 05213-0612 43170-272529
| CURRENT APPLICATION NUMBER: US/10/127,066
| CURRENT FILING DATE: 2002-07-23
| NUMBER OF SEQ ID NOS: 45
| SEQ ID NO 42
| ENGTH: 378
                                                                                                                                                                      Query Match
99.7%; Score 1535; DB 4; Length 378;
Best Local Similarity 99.6%; Pred. No. 9.3e-120;
Matches 259; Conservative 0; Mismatches 1; Indels
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; SOFTWARE: PatentIn version 3.1; SEQ ID NO 42; LENGTH: 378; TYPE: PRT; TYPE: PRT ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-10-127-066-42
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Search completed: August 29, 2006, 14:16:57 Job time : 182 secs

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